



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 138608

To: Sarvamangala Devi  
Location: REM 3C18  
Art Unit: 1645  
Tuesday, November 23, 2004  
  
Case Serial Number: 10/022832

From: Beverly Shears  
Location: Remsen Bldg.  
RM 1A54  
Phone: 571-272-2528  
  
beverly.shears@uspto.gov

### Search Notes

Shears, Beverly

From: Devi, Sarvamangala  
Sent: Tuesday, November 23, 2004 7:39 AM  
To: Shears, Beverly  
Subject: 10/022,832

Beverly:

In application 10/022,832, would you please perform a sequence search for SEQ ID NO: 2 in commercial and interference databases? Please include an inventors' name search for France Couture; Josee Hamel; Bernard R. Brodeur; Denis Martin; Pascal Brassard; Frederic Beaudoin; and Paul Prefontaine.

Thanx.

S. DEVI, Ph.D.  
AU 1645  
Rems - 3C18

Searcher: Beverly e 2528  
Terminal time: \_\_\_\_\_  
Elapsed time: \_\_\_\_\_  
CPU time: \_\_\_\_\_  
Total time: \_\_\_\_\_  
Number of Searches: \_\_\_\_\_  
Number of Databases: \_\_\_\_\_

\_\_\_\_\_ STIC

\_\_\_\_\_ CM-1

\_\_\_\_\_ Pre-S

#### Type of Search

\_\_\_\_\_ N.A. Sequence

\_\_\_\_\_ A.A. Sequence

\_\_\_\_\_ Structure

\_\_\_\_\_ Bibliographic

\_\_\_\_\_ IG

☒ STN

☒ Dialog

\_\_\_\_\_ APS

\_\_\_\_\_ Geninfo

\_\_\_\_\_ SDC

\_\_\_\_\_ DARC/Questel

\_\_\_\_\_ Other

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 23, 2004, 12:10:53 ; Search time 154 Seconds  
(without alignments)  
600.988 Million cell updates/sec

Title: US-10-022-832-2

Perfect score: 1299

Sequence: 1 MNRRLNLVLTVALLSVAS.....LIQSADEAAVPOEQNGE 258

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1299	100.0	258	2	AAY35281 Chlamydia
2	1299	100.0	258	3	AAY56993 C. pneumo
3	1299	100.0	258	5	ABB90553 Chlamydia
4	1299	100.0	258	5	ABP61993 C. pneumo
5	1250	96.2	249	3	AAY56994 C. pneumo
6	763	58.7	243	7	ADD43854 Chlamydia
7	744	57.3	250	2	AAY37675 Chlamydia
8	305.5	23.5	249	6	ADA34321 Acinetoba
9	297	22.9	272	3	AAY75136 Neisseria
10	297	22.9	272	3	AAY75787 Neisseria
11	297	22.9	272	3	AB25632 N. mening
12	297	22.9	272	3	AB58562 N. mening
13	287.5	22.1	269	3	AAY82951 BAS023 p
14	287	22.1	272	3	AAY75786 Neisseria
15	287	22.1	272	3	AAY75137 Neisseria
16	287	22.1	272	3	AAY75789 Neisseria
17	287	22.1	272	3	AAY75134 Neisseria
18	287	22.1	272	3	AB25631 N. mening
19	287	22.1	272	3	AB58564 N. mening
20	287	22.1	272	3	AB58561 N. mening
21	285	21.9	272	3	AAY75135 Neisseria
22	285	21.9	272	3	AAY75788 Neisseria
23	285	21.9	272	3	AB25633 N. gonorr
24	285	21.9	272	3	AB58563 N. gonorr
25	285	21.9	334	6	ABP77252 N. gonorr

26	284	21.9	272	3	AAB25634 N. mening
27	282.5	21.7	269	3	AAY82950 BAS023 p
28	279.5	21.5	222	3	AAY75133 Neisseria
29	279.5	21.5	222	3	AAY75784 Neisseria
30	279.5	21.5	222	3	AAB25629 N. mening
31	279.5	21.5	222	3	AAB58559 N. mening
32	269.5	20.7	255	6	ABM70454 Phototab
33	263	20.2	323	7	ABO69153 Pseudomon
34	262.5	20.2	215	3	AAY75132 Neisseria
35	262.5	20.2	215	3	AAY75785 Neisseria
36	262.5	20.2	215	3	AAB25630 N. gonorr
37	262.5	20.2	215	3	AAB58560 N. gonorr
38	253	19.5	246	6	ADA34326 Acinetoba
39	237	18.2	254	7	ABO64397 Klebsiell
40	233.5	18.0	255	7	ADF06499 Bacterial
41	233.5	18.0	270	8	ABM79751 Expressio
42	233.5	18.0	270	8	ADO14134 Chaperone
43	233	17.9	385	6	ABP71560 FkpA-gp21
44	233	17.9	537	6	ABP72251 Single ch
45	233	17.9	688	6	ABP71559 FkpAPkpAg

ALIGNMENTS

RESULT 1

AAY35281  
ID AAY35281 standard; protein; 258 AA.

AC AAY35281;

XX 17-OCT-2003 (revised)

DT 13-SEP-1999 (first entry)

XX Chlamydia pneumoniae transmembrane protein sequence.

XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;  
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;  
KW neutralising epitope.

XX Chlamydophila pneumoniae.

XX WO9927105-A2.

XX 03-JUN-1999.

XX 20-NOV-1998; 98WO-IB001890.

XX 21-NOV-1997; 97FR-00014673.

XX 04-NOV-1998; 98US-0107078P.

XX (GEST ) GENSET.

XX Griffais R;

XX WPI; 1999-357842/30.

XX Genome sequence of Chlamydia pneumoniae.

XX Page 1103-1104; Disclosure; 1912pp; English.

XX AAY34584-Y35879 represent the proteins encoded by all the open reading  
frames in the complete genome (see AAY91990) of Chlamydia pneumoniae. C.  
pneumoniae causes respiratory disease such as pneumonia and bronchitis  
and is thought to be a contributing factor in heart disease, sarcoidosis,  
sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The  
polypeptides encoded by the open reading frames of the C. pneumoniae  
genome (see AAY34584-Y35879) can be used in immunogenic compositions as  
vaccines. Vectors containing C. pneumoniae nucleotide sequences can also  
be used as immunogenic compositions, especially where the vector directs  
the expression of a neutralising epitope of C. pneumoniae. (Updated on 17  
-OCT-2003 to standardise OS field)

SQ Sequence 258 AA;  
Query Match 100.0%; Score 1299; DB 2; Length 258;  
Best Local Similarity 100.0%; Pred. No. 5.2e-118;  
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRRLNLVLTALVALSVASCDVRSKDKDQGSLSVEYKDKNDTNDIELSDNQLSRTFG 60  
DB 1 MNRRLNLVLTALVALSVASCDVRSKDKDQGSLSVEYKDKNDTNDIELSDNQLSRTFG 60

QY 61 HLLARLRKSEDMFFDIAEVAKGLQAEIVCKAPLTETEYEKMAEVOVKLVFEKSKENL 120  
DB 61 HLLARLRKSEDMFFDIAEVAKGLQAEIVCKAPLTETEYEKMAEVOVKLVFEKSKENL 120

QY 121 SLAEKFLKSNKAGVVEVQPSKLYKIIKEGAGKAIISGKPSALLHYKGSFINGQVFS 180  
DB 121 SLAEKFLKSNKAGVVEVQPSKLYKIIKEGAGKAIISGKPSALLHYKGSFINGQVFS 180

QY 181 EGNNEPILLPLGQTIPGFALGMQMGKEGTRVLYIHPDLAYGTAGOLPPNSLLIFEINLI 240  
DB 181 EGNNEPILLPLGQTIPGFALGMQMGKEGTRVLYIHPDLAYGTAGOLPPNSLLIFEINLI 240

QY 241 QASADEVAAPVQEGNOGE 258  
DB 241 QASADEVAAPVQEGNOGE 258

RESULT 2  
ID AAY56993 standard; protein; 258 AA.  
AC AAY56993;  
XX AAY56993;  
DT 12-SEP-2003 (revised)  
DT 08-MAY-2000 (first entry)  
XX C. pneumoniae mip (outer membrane protein).  
XX Chlamydia pneumoniae; outer membrane protein; mip; CPN100501;  
KW Chlamydial infection.  
XX Chlamydia pneumoniae.  
XX W0200006741-A1.  
XX 10-FEB-2000.  
XX 27-JUL-1999; 99WO-IB001330.  
XX 27-JUL-1998; 98US-0094192P.  
XX 01-MAR-1999; 99US-0122044P.  
XX 26-JUL-1999; 99US-00361440.  
XX (CONN-) CONNAUGHT LAB LTD.  
XX Murdin AD, Oomen RP, Dunn PL;  
XX WPI; 2000-195302/17.  
XX N-PSDB; AAZ56942.  
XX Novel polynucleotides and Chlamydia pneumoniae outer membrane protein  
XX encoded by them for use as vaccines in treating and diagnosing chlamydial  
XX infections.  
XX Claim 6; Fig 1A-C; 55pp; English.  
XX The invention provides an isolated polynucleotide encoding Chlamydia  
XX pneumoniae outer membrane protein (mip or CPN100501). The mip protein can  
XX be expressed by standard recombinant methodology. The mip gene is used  
XX for detecting Chlamydia by hybridizing or amplifying the sample with the  
XX mip gene specific probe. A vaccine vector or a pharmaceutical composition  
XX comprising the mip gene are used for inducing an immune response in a  
XX mammal to prevent/treat chlamydial infections particularly infections

CC caused by C. pneumoniae. The present sequence represents the amino acid  
CC sequence of the C. pneumoniae full-length mip protein. (Updated on 12-SEP  
XX -2003 to standardise OS field)  
SQ Sequence 258 AA;  
Query Match 100.0%; Score 1299; DB 3; Length 258;  
Best Local Similarity 100.0%; Pred. No. 5.2e-118;  
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRRLNLVLTALVALSVASCDVRSKDKDQGSLSVEYKDKNDTNDIELSDNQLSRTFG 60  
DB 1 MNRRLNLVLTALVALSVASCDVRSKDKDQGSLSVEYKDKNDTNDIELSDNQLSRTFG 60

QY 61 HLLARLRKSEDMFFDIAEVAKGLQAEIVCKAPLTETEYEKMAEVOVKLVFEKSKENL 120  
DB 61 HLLARLRKSEDMFFDIAEVAKGLQAEIVCKAPLTETEYEKMAEVOVKLVFEKSKENL 120

QY 121 SLAEKFLKSNKAGVVEVQPSKLYKIIKEGAGKAIISGKPSALLHYKGSFINGQVFS 180  
DB 121 SLAEKFLKSNKAGVVEVQPSKLYKIIKEGAGKAIISGKPSALLHYKGSFINGQVFS 180

QY 181 EGNNEPILLPLGQTIPGFALGMQMGKEGTRVLYIHPDLAYGTAGOLPPNSLLIFEINLI 240  
DB 181 EGNNEPILLPLGQTIPGFALGMQMGKEGTRVLYIHPDLAYGTAGOLPPNSLLIFEINLI 240

QY 241 QASADEVAAPVQEGNOGE 258  
DB 241 QASADEVAAPVQEGNOGE 258

RESULT 3  
ID ABB90553 standard; protein; 258 AA.  
XX ABB90553;  
AC ABB90553;  
XX ABB90553;  
DT 29-AUG-2003 (revised)  
DT 29-JUL-2002 (first entry)  
XX Chlamydia pneumoniae cp6960 protein, SEQ ID NO:55.  
DE Chlamydial infection; antigen; immunogen; vaccine; diagnosis;  
XX human respiratory disease; cardiovascular disease; atherosclerosis;  
KW coronary artery disease; carotid artery stenosis; myocardial infarction;  
KW cerebrovascular disease; aortic aneurysm; claudication; stroke;  
KW strain CWL029.  
XX Chlamydia pneumoniae.  
XX Key Location/Qualifiers  
FH Peptide 1..25 /label= Signal\_peptide  
FT Protein 26..258 /note= "Mature protein"  
XX W0200202606-A2.  
XX 10-JAN-2002.  
XX 03-JUL-2001; 2001WO-IB001445.  
XX 03-JUL-2000; 2000GB-00016363.  
XX 11-JUL-2000; 2000GB-00017047.  
XX 21-JUL-2000; 2000GB-00017983.  
XX 07-AUG-2000; 2000GB-00019368.  
XX 18-AUG-2000; 2000GB-00020440.  
XX 14-SEP-2000; 2000GB-00022583.  
XX 10-NOV-2000; 2000GB-00027549.  
XX 22-DEC-2000; 2000GB-00031706.  
XX (CHIR-) CHIRON SPA.  
XX

PI Ratti G, Grandi G;  
 DR WPI; 2002-154726/20.  
 DR N-PSDB; ABL91211.  
 XX  
 XX Novel Chlamydia pneumoniae protein useful in the manufacture of a  
 PT medicament for treatment or prevention of infection due to Chlamydia,  
 PT preferably Chlamydia pneumoniae, and for diagnostic purposes.  
 XX  
 XX Claim 1; Page 69; 364pp; English.  
 XX  
 XX Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia  
 CC pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding  
 CC them. The proteins are predicted to be immunogenic and may therefore be  
 CC useful in vaccine production and for diagnostic purposes. Chlamydia  
 CC pneumoniae is a common cause of respiratory disease in humans, and is  
 CC also involved in the development of cardiovascular diseases such as  
 CC atherosclerosis, coronary artery disease, carotid artery stenosis,  
 CC myocardial infarction, cerebrovascular disease, aortic aneurysm,  
 CC claudication and stroke. The proteins and nucleic acids of the invention  
 CC may be used in vaccines and pharmaceutical compositions for the  
 CC prevention or treatment of chlamydial infections, particularly Chlamydia  
 CC pneumoniae infections. The proteins may also be used in the detection of  
 CC Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched  
 CC DNA probe assay or blotting techniques for determining Chlamydia  
 CC pneumoniae gene expression. The present sequence represents a  
 CC specifically claimed Chlamydia pneumoniae protein of the invention.  
 CC (Updated on 29-AUG-2003 to standardise OS field)  
 XX  
 XX Sequence 258 AA;  
 SQ  
 Query Match 100.0%; Score 1299; DB 5; Length 258;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-118;  
 Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNRWNVLVATVALSASCDVRSKDKDQGSILVEYKDKNDNDIELSDNQLSRTFG 60  
 DB 1 MNRWNVLVATVALSASCDVRSKDKDQGSILVEYKDKNDNDIELSDNQLSRTFG 60  
 QY 61 HLLARQLRKSDEMFDDIAEVAKGLQAEVLVCKSAPLTETETEYEEKMAEVQKLVFEKSKENL 120  
 DB 61 HLLARQLRKSDEMFDDIAEVAKGLQAEVLVCKSAPLTETETEYEEKMAEVQKLVFEKSKENL 120  
 QY 121 SLAEKFLKENSKNAGVVEVQPSKLYKIIEGAGKAIISGKPSALLHYKGSFINGQVFS 180  
 DB 121 SLAEKFLKENSKNAGVVEVQPSKLYKIIEGAGKAIISGKPSALLHYKGSFINGQVFS 180  
 QY 181 EGNNEPILLPLGQTTIPGALGMOGKGETRVLVYHPDLAYGTAGQLPPNLLIFEINLI 240  
 DB 181 EGNNEPILLPLGQTTIPGALGMOGKGETRVLVYHPDLAYGTAGQLPPNLLIFEINLI 240  
 QY 241 QASADEVAAPVQEGNQGE 258  
 DB 241 QASADEVAAPVQEGNQGE 258  
 RESULT 4  
 ID ABP61993 standard; protein; 258 AA.  
 XX  
 AC ABP61993;  
 XX  
 DT 29-AUG-2003 (revised)  
 DT 08-OCT-2002 (first entry)  
 XX  
 DE C. pneumoniae BVH-CPN1 from strain CWL-029.  
 XX  
 CWL-029; BVH-CPN; antibiotic; antibacterial; Chlamydial infection;  
 KW sinusitis; pharyngitis; bronchitis; pneumonitis; asthmatic bronchitis;  
 KW adult-onset asthma; chronic obstructive pulmonary disease; COPD;  
 KW atherogenesis; atherosclerosis.  
 XX  
 OS Chlamydophila pneumoniae.

XX Key Location/Qualifiers  
 FH Peptide 1..20  
 FT /label= Leader\_peptide  
 FT Protein 21..258  
 FT /label= Mature\_BVH-CPN1  
 XX EPI219635-A2.  
 XX 03-JUL-2002.  
 XX 21-DEC-2001; 2001EP-00130295.  
 XX 21-DEC-2000; 2000US-0256941P.  
 XX (SHIR-) SHIRE BIOCHEM INC.  
 PI Couture F, Hamel J, Brodeur BR, Martin D;  
 DR WPI; 2002-530680/57.  
 DR N-PSDB; ABQ92487.  
 XX  
 XX New Chlamydia pneumoniae proteins or antigens, useful for the  
 PT prophylactic or therapeutic treatment of Chlamydial bacterial infections,  
 PT e.g. sinusitis, pharyngitis, bronchitis, or chronic obstructive pulmonary  
 PT disease.  
 XX  
 XX Claim 9; Fig 2; 122pp; English.  
 XX  
 XX The invention relates to novel isolated polypeptides from Chlamydia  
 CC pneumoniae. The polypeptides of the invention have antibiotic and  
 CC antibacterial activity. The polypeptide or composition of the invention  
 CC is useful for the prophylactic or therapeutic treatment of Chlamydial  
 CC bacterial infection (specifically those caused by C. pneumoniae, C.  
 CC psittaci or C. trachomatis), e.g. sinusitis, pharyngitis, bronchitis,  
 CC pneumonitis, asthmatic bronchitis, adult-onset asthma, chronic  
 CC obstructive pulmonary disease (COPD), atherogenesis or atherosclerosis.  
 CC The sequences shown in ABP61993-ABP62011 represent proteins BVH-CPN1 to  
 CC BVH-CPN19 of C. pneumoniae. (Updated on 29-AUG-2003 to standardise OS  
 CC field)  
 XX  
 XX Sequence 258 AA;  
 SQ  
 Query Match 100.0%; Score 1299; DB 5; Length 258;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-118;  
 Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNRWNVLVATVALSASCDVRSKDKDQGSILVEYKDKNDNDIELSDNQLSRTFG 60  
 DB 1 MNRWNVLVATVALSASCDVRSKDKDQGSILVEYKDKNDNDIELSDNQLSRTFG 60  
 QY 61 HLLARQLRKSDEMFDDIAEVAKGLQAEVLVCKSAPLTETETEYEEKMAEVQKLVFEKSKENL 120  
 DB 61 HLLARQLRKSDEMFDDIAEVAKGLQAEVLVCKSAPLTETETEYEEKMAEVQKLVFEKSKENL 120  
 QY 121 SLAEKFLKENSKNAGVVEVQPSKLYKIIEGAGKAIISGKPSALLHYKGSFINGQVFS 180  
 DB 121 SLAEKFLKENSKNAGVVEVQPSKLYKIIEGAGKAIISGKPSALLHYKGSFINGQVFS 180  
 QY 181 EGNNEPILLPLGQTTIPGALGMOGKGETRVLVYHPDLAYGTAGQLPPNLLIFEINLI 240  
 DB 181 EGNNEPILLPLGQTTIPGALGMOGKGETRVLVYHPDLAYGTAGQLPPNLLIFEINLI 240  
 QY 241 QASADEVAAPVQEGNQGE 258  
 DB 241 QASADEVAAPVQEGNQGE 258  
 RESULT 5  
 ID AAY56994 standard; protein; 249 AA.  
 XX  
 AC AAY56994;

```
XX 12-SEP-2003 (revised)
DT 08-MAY-2000 (first entry)
XX
XX C. pneumoniae mip (outer membrane protein) truncated protein.
XX
XX Chlamydia pneumoniae; outer membrane protein; mip; CPN100501;
KW Chlamydial infection.
XX
XX Chlamydia pneumoniae.
XX
XX WO200006741-A1.
XX
XX 10-FEB-2000.
XX
XX 27-JUL-1999; 99WO-IB001330.
XX
XX 27-JUL-1998; 98US-0094192P.
PR 01-MAR-1999; 99US-0122044P.
PR 26-JUL-1999; 99US-00361440.
XX
XX (CONN-) CONNAUGHT LAB LTD.
XX
XX Murdin AD, Oomen RP, Dunn PL;
XX
XX WPI; 2000-195302/17.
DR N-PSDB; AAZ56942.
XX
XX Novel polynucleotides and Chlamydia pneumoniae outer membrane protein
PT encoded by them for use as vaccines in treating and diagnosing chlamydial
PT infections.
XX
XX Claim 5; Fig 1A-C; 55pp; English.
XX
XX The invention provides an isolated polynucleotide encoding Chlamydia
CC pneumoniae outer membrane protein (mip or CPN100501). The mip protein can
CC be expressed by standard recombinant methodology. The mip gene is used
CC for detecting Chlamydia by hybridizing or amplifying the sample with the
CC mip gene specific probe. A vaccine vector or a pharmaceutical composition
CC comprising the mip gene are used for inducing an immune response in a
CC mammal to prevent/treat chlamydial infections particularly infections
CC caused by C. pneumoniae. The present sequence represents the amino acid
CC sequence of the C. pneumoniae truncated mip protein. (Updated on 12-SEP-
CC 2003 to standardise OS field)
XX
XX SQ Sequence 249 AA;
XX
XX Query Match 96.2%; Score 1250; DB 3; Length 249;
XX Best Local Similarity 100.0%; Pred. No. 3e-113;
XX Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MNRNRNLVATVALALSVASCDVRSKDKDQGSLEYKDKNDTNDIELSDNOKLSRTFG 60
DB 1 MNRNRNLVATVALALSVASCDVRSKDKDQGSLEYKDKNDTNDIELSDNOKLSRTFG 60
XX
QY 61 HLLARQLRKSEDMFDDIAEVAKGLQAEVLVCKSAPLTETEEYKMAEYQKLVFEKSKENL 120
DB 61 HLLARQLRKSEDMFDDIAEVAKGLQAEVLVCKSAPLTETEEYKMAEYQKLVFEKSKENL 120
XX
QY 121 SLAEKFLKENSKNAGVVEVQPSKLYKIIKEGAGKAIKSGKPSALLHYKGSFINGQVPS 180
DB 121 SLAEKFLKENSKNAGVVEVQPSKLYKIIKEGAGKAIKSGKPSALLHYKGSFINGQVPS 180
XX
QY 181 EGNNEPILLPLGQITPGFALGCMQKGETRVLVIHPDLAYGTAGOLPPNLSLIFEINLI 240
DB 181 EGNNEPILLPLGQITPGFALGCMQKGETRVLVIHPDLAYGTAGOLPPNLSLIFEINLI 240
XX
QY 241 QASADEVAA 249
DB 241 QASADEVAA 249
XX
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ADD43854
ID ADD43854 standard; protein; 243 AA.
XX
AC ADD43854;
XX
XX 15-JAN-2004 (first entry)
XX
XX Chlamydia trachomatis immunogenic protein, SEQ ID NO 149.
XX
XX immunogenic; infection; Chlamydia trachomatis; immune; vaccine;
KW gene therapy; antibacterial.
XX
XX Chlamydia trachomatis.
XX
XX WO2003049762-A2.
XX
XX 19-JUN-2003.
XX
XX 12-DEC-2002; 2002WO-IB005761.
XX
XX 12-DEC-2001; 2001GB-00029732.
PR 06-AUG-2002; 2002GB-00018233.
PR 14-AUG-2002; 2002GB-00018924.
XX
XX (CHIR-) CHIRON SPA.
XX
XX Grandi G, Ratti G;
XX
XX WPI; 2003-532882/50.
DR N-PSDB; ADD43855.
XX
XX New immunogenic composition having a protein or encoding nucleic acid,
PT useful for diagnosing, preventing and/or treating Chlamydia trachomatis
PT infection.
XX
XX Claim 6; SEQ ID NO 149; 164pp; English.
XX
XX The invention relates to a novel immunogenic composition comprising a
CC protein or nucleic acid, and an adjuvant, where the protein or nucleic
CC acid comprises any of 131 fully defined amino acid or nucleotide
CC sequences given in the specification, or has 50% or greater sequence
CC identity to it, or their fragments. The protein and/or nucleic acid of
CC the immunogenic composition is useful in the manufacture of a medicament
CC for the treatment or prevention of infection due to Chlamydia
CC trachomatis. The infection is treated or prevented by the medicament
CC eliciting an immune response which is specific to a C. trachomatis
CC elementary body, or for neutralising C. trachomatis elementary bodies,
CC hence the immunogenic composition can be used in creating a vaccine. The
CC immunogenic compositions can also be used for the diagnosis of C.
CC trachomatis infection. The nucleic acids of the immunogenic compositions
CC can be used to treat disorders by gene therapy. The immunogenic
CC compositions have antibacterial activity. This sequence represents one of
CC the 131 C. trachomatis proteins with immunogenic properties of the
CC invention.
XX
XX SQ Sequence 243 AA;
XX
XX Query Match 58.7%; Score 763; DB 7; Length 243;
XX Best Local Similarity 61.1%; Pred. No. 9.8e-66;
XX Matches 149; Conservative 36; Mismatches 49; Indels 10; Gaps 2;
XX
QY 5 WNLVLATVALALSVASCDVRSKDKDQGSLEYKDKNDTNDIELSDNOKLSRTFGHLLA 64
DB 7 WMLMF---AVALPIVGC-----DNGGGSOTSATEKSMVEDSALTNDNOKLSRTFGHLLS 56
XX
QY 65 RQLRKSEDMFDDIAEVAKGLQAEVLVCKSAPLTETEEYKMAEYQKLVFEKSKENLSLAE 124
DB 57 RQLSRTEFSLDLVEVIKGMQSEIDQGSAPLTDTEYKMAEYQKASFEAKCSENLSAE 116
XX
QY 125 KFLKENSKNAGVVEVQPSKLYKIIKEGAGKAIKSGKPSALLHYKGSFINGQVPSSEGN 184
DB 117 KFLKENKAGVIELEPNKLYRVVKEGTGRVLSGKPTALLHYTGSFDGKRVFDSSEKNK 176
XX
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QY 185 EPILLPLGOTIPGFALGMOGKEGETRVLVYHPDLAYGTAGOLPNSLLIFPEINLIQASA 244
Db 177 EPILLPLTKVIPGFSGMOGKEGEVRVLYIHPDLAYGTAGOLPNSLLIFPEVKLIEAND 236
QY 245 DEVA 248
Db 237 DNVS 240

RESULT 7
ID AAY37675 standard; protein; 250 AA.
XX AAY37675;
AC AAY37675;
DT 07-OCT-1999 (first entry)
XX Chlamydia trachomatis surface exposed protein.
DE Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis;
KW bartholinitis; pneumonia; venereal lymphogranulomatosis.
XX Chlamydia trachomatis.
OS Chlamydia trachomatis.
XX WO9928475-A2.
PN 10-JUN-1999.
PD 27-NOV-1998; 98WO-IB001939.
XX 28-NOV-1997; 97FR-00015041.
PR 17-DEC-1997; 97FR-00016034.
PR 04-NOV-1998; 98US-0107077P.
XX (GEST ) GENSET.
PA Griffais R;
PI WPI; 1999-371125/31.
DR Genome sequence of Chlamydia trachomatis.
XX Disclosure; Page 1302-1304; 1755pp; English.
CC AAY3675A-Y37949 are encoded by open reading frames (ORFs) of the genome
CC of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as
CC vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences
CC can also be used to control growth of the microorganism. Chlamydia
CC trachomatis is responsible for a large number of diseases, e.g. eye
CC diseases such as conventional trachoma, nonendemic trachoma,
CC paratrachoma, and inclusion conjunctivitis; genital diseases such as
CC nongonococcal urethritis, epididymitis, cervicitis, salpingitis,
CC perinephritis, bartholinitis; pneumopathy in breast feeding infants; and
CC venereal lymphogranulomatosis. The polypeptides of the invention may be
CC of use in treating these diseases
XX Sequence 250 AA;
SQ Query Match 57.3%; Score 744; DB 2; Length 250;
Best Local Similarity 60.2%; Pred. No. 7.3e-64;
Matches 147; Conservative 36; Mismatches 51; Indels 10; Gaps 2;
QY 5 WNLVLTVALALSVASCDVRSKDKQDQGLSVEYKDKNDTNDIELSDNOKLSRTFGHLLA 64
Db 14 WLMF---AVALPIVGC-----DNGGGSQTSATEKSMVEDSALTDNOKLSRTFGHLLA 63
QY 65 ROLRSEDMFFDIAEVAKQLAELVCKSAPLTETEEKMAEVQKLVFEKSKENLSLAE 124
Db 64 ROLRTEDESLDVEIKGMQSEIDGQSAPLTDTYEKMAEVQKASFEAKSENLSAE 123
QY 125 KFLKENSKNAGVVEVQPSKLYKIIKEGAGKAIKSGPSALLHYKGSFINGQVFSSEGN 184
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Db 124 EFLKENKEKAGVIELEPNKQYRVVKEGTGRALSGKPTALLHYTGSFDGKDFDSEKNK 183
QY 185 EPILLPLGOTIPGFALGMOGKEGETRVLVYHPDLAYGTAGOLPNSLLIFPEINLIQASA 244
Db 184 AAILPLTKVIPGFSGMOGKEGEVRVLYIHPDLAYGTAGOLPNSLLIFPEVKLIEAND 243
QY 245 DEVA 248
Db 244 DNVS 247

RESULT 8
ID ADA34321 standard; protein; 249 AA.
XX ADA34321;
AC ADA34321;
DT 20-NOV-2003 (first entry)
XX Acinetobacter baumannii protein #1482.
DE Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;
KW plant biocontrol agent.
KW Acinetobacter baumannii.
OS Acinetobacter baumannii.
XX US6562958-B1.
PN 13-MAY-2003.
PD 04-JUN-1999; 99US-00328352.
XX 09-JUN-1998; 98US-0088701P.
PR (GENO-) GENOME THERAPEUTICS CORP.
XX Breton G, Bush D;
PI WPI; 2003-576092/54.
DR N-PSDB; ADA30195.
XX New Acinetobacter baumannii proteins and nucleic acids, useful as reagents
PT for diagnosing a bacterial disease, as components of antibacterial
PT vaccines, as targets for antibacterial drugs, or as biocontrol agents for
PT plants.
XX Example; SEQ ID NO 5608; 328pp; English.
PS The invention relates to isolated Acinetobacter baumannii nucleic acids.
CC The A. baumannii nucleic acids and polypeptides are useful as reagents
CC for diagnosing a bacterial disease, as components of antibacterial
CC vaccines, as targets for antibacterial drugs, to detect the presence of
CC A. baumannii and other Acinetobacter species in a sample, in screening
CC compounds for the ability to interfere with the A. baumannii life cycle
CC or to inhibit A. baumannii infection, and as biocontrol agents for
CC plants. The present sequence represents the amino acid sequence of an A.
CC baumannii protein.
XX Sequence 249 AA;
SQ Query Match 23.5%; Score 305.5; DB 6; Length 249;
Best Local Similarity 32.7%; Pred. No. 4.6e-21;
Matches 82; Conservative 45; Mismatches 87; Indels 37; Gaps 7;
QY 3 RRNLVLTVALALSV-ASCDVRSKDKQDQGLSVEYKDKNDTNDIELSDNOKLSRTFGH 61
Db 20 KKSILVIAASTMSLSVFAAAPITNKSPAKDQ-----FSSYGY 57
QY 62 LLARQLRKS-EDMFFDIAEVAKQLAELVCKSAPLTETE-----YEEKMAEVQKLVFE 113
Db 58 LMGRNNTDALTDLNLDI---FYQGLQEGAGNQNTARTLDEMAKAINDYKRTLEAKQLVFEQ 115
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Qy	114	KSKKENLSLAERFLKENSQVAGVEQSPKLOYKIIKEGAGKAISGKPSALLHYKGSFIN	173
		: : :          :           :           :           :	
Db	116	KQGGQNAQAAGAAFLAENAKSGVWVTK-SGLQYQVLKEGSGKTPKATSRVKVNYEGRLLD	174
		: : :          :           :           :           :	
Qy	174	GOVFSSSEGNNEPILLPLGOTIPGFALGMQGMKEGTRVLVHPDLAYGTAG---OLPPN	230
		: : :          :           :           :           :	
Db	175	GIVFOSSIARNHPVDFQLNOVITAGWTEGLQTMKEGGKTRFIPAKLAYGEVGAGDSIGPN	234
		: : :          :           :           :           :	
Qy	231	SLLIFEINLIQ 241	
		:           :           :           :	
Db	235	STLIFDIELLQ 245	
		:           :           :           :	
RESULT 9			
AAV75136			
AA	ID	AAV75136 standard; protein; 272 AA.	
XX	AC	AAV75136;	
XX			
DT	21-MAR-2000	(first entry)	
XX			
DE	XX	Neisseria meningitidis ORF 576 protein sequence SEQ ID NO:1746.	
XX			
KW	XX	Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;	
KW	KW	antigenic; diagnosis; immunogenic; infection; meningitis; septicemia;	
KW	KW	antibacterial; gene therapy.	
XX			
OS	XX	Neisseria meningitidis.	
XX			
PN	XX	WO9957280-A2.	
XX			
PD	XX	11-NOV-1999.	
XX			
PF	30-APR-1999;	99WO-US009346.	
XX			
PR	01-MAY-1998;	98US-00837589.	
PR	31-JUL-1998;	98US-0094869P.	
PR	02-SEP-1998;	98US-0096994P.	
PR	02-SEP-1998;	98US-0099062P.	
PR	03-OCT-1998;	98US-0103749P.	
PR	03-OCT-1998;	98US-0103794P.	
PR	03-OCT-1998;	98US-0103796P.	
PR	25-FEB-1999;	99US-0121528P.	
XX			
PA	(CHIR )	CHIRON CORP.	
PA	(GENO- )	INST GENOMIC RES.	
XX			
PI	Fraser C, Galocetti C, Grandi G, Hickey E, Maignani V, Mora M;		
PI	Petersen J, Piazza M, Rappuoli R, Ratti G, Scalato E, Scarselli M;		
PI	Tettelin H, Venter JC;		
XX			
DR	WPI;	2000-062150/05.	
DR	N-PSDB;	AA253898.	
XX			
PT	Novel Neisserial polypeptides predicted to be useful antigens for		
PT	vaccines and diagnostics.		
XX			
PS	Claim 2;	Page 892; 1453pp; English.	
XX			
CC	AAZ53015	to AAZ54536, AAZ54577 to AAZ54615, and AAV74253 to AAV75941	
CC	represent novel Neisseria meningitis and N, gonorrhoea polynucleotides		
CC	and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ5473 represent		
CC	PCR primers used in the exemplification of the present invention. The		
CC	polypeptides, the polynucleotides, antibodies and compositions of the		
CC	invention can be used as vaccines, as diagnostic reagents, and as		
CC	immunogenic compositions. The polypeptides can be used in the manufacture		
CC	of medicaments for treating or preventing infection due to Neisserial		
CC	bacteria (e.g. meningitis and septicemia), to detect the presence of		
CC	Neisseria bacteria, or to raise antibodies. They may also be used to		
CC	screen for agonists or antagonists, which may themselves have use as		
CC	antibacterial agents. The polynucleotides of the invention may also be		
CC	used in gene therapy protocols		
XX			



AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel *Neisseria meningitis* and *N. gonorrhoeae* polynucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to *Neisseria* bacteria (e.g. *meningitis* and *septicaemia*), to detect the presence of *Neisseria* bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols

Query Match	22.9%;	Score	297;	DB	3;	Length	272;
Best Local Similarity	31.8%;	Pred. No.	3.5e-20;				
Matches	84;	Conservative	42;	Mismatches	124;	Indels	14;
						Gaps	6;

  

QY	1	MNRWNVLVATVALALSVASCDVRSKDKDKDQGSILVEYKDNKNTDNTELSDNQKLSRTFG	60
DB	1	MNTIFKISALTLSAALASCGKKEAPASAPASAPAAASSAQGDTSISIG-STWQQASYAMG	59
QY	61	HLLARQLR--KSEDMFFDIAEAVKGLQAEIVCKSAPIETETIEYERK-----AEVKLIVFEK	114
DB	60	VDIGRSLSQMKQEQAEDLKVFTTEAMQAVDVGKEIKMTTEQAQVMMKMFLOEQQAKAVEK	119
QY	115	---KSKENLSLAEBKXENSKNAGVWEVQPSKLOYKIIKEGAGKAISGKPSALLHYKGSF	171
DB	120	HKADAKANKEGEAFLENAAKDG-VKTTASGLQYKITKGEGKQPTKDDIVTVEYEGRL	178
QY	172	INQGVFSSSGNNIEPILLPGITPGFALGMQGNKEGETRVLYIHPDLAY---GTAGQLP	228
DB	179	IDGTVPDSSKANGGFVTFPSQVIFPGTWGTVQLLKEGGEATFIPSNLAYREQAGDKIG	238
QY	229	PNSLLIPEINL1QASADEVAAPVQ	252
DB	239	PNATLVEDVKLVKIGAPENAPAKO	262

RESULT 11	
AA25632	
ID	AA25632 standard; protein; 272 AA.
XX	
AC	AA25632;
XX	
DT	04-DEC-2000 (first entry)
XX	
DE	N. meningitidis amino acid sequence m576-1.pep SEQ ID NO:987.
DE	
KW	Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;
KW	antigen; vaccine; diagnosis; infection; antibacterial; identification;
KW	Meningococcus B; MenB.
XX	
OS	Neisseria meningitidis.

XX	WO200022430-A2.	
PN	XX	
XX	20-APR-2000.	
PD	XX	
XX	08-OCT-1999; 99WO-US023573.	
PF	XX	
XX	09-OCT-1998; 98US-0103794P.	
PR	30-APR-1999; 99US-0132068P.	
XX	(CHIR ) CHIRON CORP.	
PA	XX	
XX	Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;	
PI	PI Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;	
PI	PI Rappuoli R, Pizza M;	
XX	WPI; 2000-318079/27.	
XX		
DR		

N-PSDB; AAA81272.

Isolated nucleotide sequences of *Neisseria meningitidis* which can be used in the diagnosis and treatment of *N. meningitidis* infection and other *Neisseria* infections, for example, *N.gonorrhoea*.

Claim 14; Page 78; 1760pp; English.

The present invention describes methods of obtaining immunogenic proteins from *Neisseria* genomic sequences. AAA81453 to AAA82414 represent specifically claimed *Neisseria meningitidis* genomic DNA sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent *Neisseria* DNA sequences and their corresponding proteins; AAA81254 to AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the isolation of *Neisseria meningitidis* DNA sequences; and AAA81322 to AAA81452 represent *Neisseria meningitidis* MenB polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to *Neisseria* bacteria. For example, some of the identified proteins could be components of vaccines against *Meningococcus B*; against all serotypes; and/or against all pathogenic *Neisseriae*. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious *Meningococcus B* vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than other more variable regions

Sequence 272 AA;

Query Match	22.9%	Score 297;	DB 3;	Length 272;
Best Local Similarity	31.8%	Pred. No. 3.5e-20;		
Matches	84;	Conservative 42;	Mismatches 124;	Indels 14; Gaps 6

  

Qy	1	MNRWNLVLATVALALSVASCDVFSKOKDKQGSVLEYKDNKNDTNDIELSDNQKLSRTFG	60
Db	1	MNTIFKLSALTSLAALASACGCKEAPASAPASAAQGDTSIG-STWQQAAYANG	59
Qy	61	HLLARQLR--KSDMFFDIAEAVKGLQAEVLCKSAPLTETEEYK-----AEVQKLVPKE	114
Db	60	VDIGRSUKOMKEQGAEDLKVFTETAMQAVYCKEITBEQAEVMMKFLQEQQAKAVKE	119
Qy	115	---KSKENLSLAERFLKENSKNAGVVEVQPSKLYKIIKEGAKGAIKSPSALLHYKGSF	171
Db	120	HKADAKANKEGEAFLKENAAKDG-VKTTASGLQYKITKGEGKQPTKDDIVTVEYEGRL	178
Qy	172	INGQVFSSEGNNEPILPLPQOTIPGFALGMQMKGETRVLVIHPDLAY----GTAGQQLP	228
Db	179	IDGTVDFSSKANGGVPVTPLSQVIPGMWTEGVQLLKEGGGEATYFIPSNLAYREQAGDKIG	238
Qy	229	PNSLLIFEINLIQASADEVAAPQ	252
Db	239	PNATLVDFDKLVKIGAPENAPAKQ	262

RESULT 12	
AAB58562	
ID	AAB58562 standard; protein; 272 AA.
XX	
XX	
AC	AAB58562;
XX	
XX	
DT	13-MAR-2001 (first entry)
XX	
XX	
XX	N. meningitidis amino acid sequence m576-1.pep SEQ ID NO:27.
DE	
XX	
XX	Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;
KW	diagnosis; antigen; detection; infection; gene therapy; antibacterial.
KW	



Db 1 MNTIFKISAITLSAALALSACGKKEAPASASEPAAASSAAGDTSISIG-STWQQASYANG 59

Qy 61 HLARQLR--KSEDMFFDIAEVAAGLQALVCKASPLTETETVEEKK- ---AEVQKLVPFK 114

Db 60 VDIGRSLKQMKEQGAETDLKVFTTEAMQAVYDGKEIKWTEEQAEVMMKFLQEQQAKAVEK 119

Qy 115 ---KSKENLSLAEKFLKENSKNAGVEVQPSKLOYKIIKEGAGKAKAISGPSALLHYKGSF 171

Db 120 HKADAKANKKEGAFLKENAAKDG-VKTTASGLQYKITKQEGKQPTKDDIVTVEYEGRL 178

Qy 172 INGVQFSSSGNNEPILLPLGOTIPGFALGMQWKEGSTRVLYIHPDLAY---GTAGQLP 228

Db 179 IDGTVFSSKANGGVFTPLPSQVILGWTGEGVQLLKEGGEATFIPSNLAYREQAGDKIG 238

Qy 229 PNSLLIFEINLIQASADEVAAPVQ 252

Db 239 PNATLVFDVKLVKIGAPENAPAKQ 262

RESULT 15

AAV75137 ID AAY75137 standard; protein; 272 AA.

XX AC AAY75137;

XX DT 21-MAR-2000 (first entry)

XX NEisseria meningitidis ORF 576 protein sequence SEQ ID NO:1748.

DE NEisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;

XX KW antigenic; diagnosis; Neisseria gonorrhoeae; infection; meningitis; septicemia;

KW antibacterial; gene therapy.

XX OS Neisseria meningitidis.

XX PN WO9957280-A2.

XX PD 11-NOV-1999.

XX PF 30-APR-1999; 99WO-US009346.

XX PR 01-MAY-1998; 98US-0083758P.

PR 31-JUL-1998; 98US-0094869P.

PR 02-SEP-1998; 98US-0098994P.

PR 02-SEP-1998; 98US-0099062P.

PR 09-OCT-1998; 98US-0103749P.

PR 09-OCT-1998; 98US-0103794P.

PR 09-OCT-1998; 98US-0103796P.

PR 25-FEB-1999; 99US-0121528P.

XX (CHIR ) CHIRON CORP.

PA (GENO-) INST GENOMIC RES.

PA Fraser C, Galeotti C, Grandi G, Hickey E, Massignani V, Mora M;

PI Petersen J, Piazza M, Rappuoli R, Ratti G, Scialato E, Scarselli M;

PI Tettelin H, Venter JC;

XX WPI; 2000-062150/05.

DR N-PSDB; AAZ53899.

XX Novel Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics.

PS Claim 2; Page 893; 1453pp; English.

XX AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrhoea polynucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 23, 2004, 12:10:53 ; Search time 39 Seconds  
(without alignments)  
438.719 Million cell updates/sec

Title: US-10-022-832-2

Perfect score: 1299

Sequence: 1 MNRWNLVLTVALSAS.....LIQASDEVAAPQEGNQGE 258

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pap.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pap.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pap.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pap.\*
- 5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pap.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1299	100.0	258	4	US-09-198-452A-699
2	305.5	23.5	249	4	US-09-328-352-5608
3	287.5	22.1	269	4	US-09-762-878-4
4	282.5	21.7	269	4	US-09-762-878-2
5	263	20.2	323	4	US-09-252-991A-17899
6	253	19.5	246	4	US-09-328-352-5613
7	237	18.2	254	4	US-09-489-039A-10914
8	233.5	18.0	255	4	US-09-543-681A-6784
9	226	17.4	239	4	US-09-809-665A-143
10	219	16.9	218	4	US-09-252-991A-21404
11	185.5	14.3	223	4	US-09-543-681A-5818
12	167.5	12.9	257	4	US-09-489-039A-8908
13	160	12.3	157	4	US-09-270-767-44323
14	159	12.2	107	3	US-08-894-173-69
15	159	12.2	107	3	US-08-894-173-83
16	159	12.2	107	3	US-09-398-193-69
17	159	12.2	107	3	US-09-398-193-83
18	159	12.2	119	5	PCT-US92-03993-1
19	159	12.2	120	1	US-08-336-618-17
20	156	12.0	412	2	US-08-741-134-2
21	150.5	11.6	230	4	US-09-481-620A-111
22	150	11.5	107	3	US-08-894-173-82
23	150	11.5	107	3	US-09-398-193-82
24	150	11.5	108	3	US-08-714-071-1
25	149.5	11.5	137	4	US-09-481-620A-85
26	149	11.5	107	1	US-08-197-795-2
27	149	11.5	107	1	US-08-336-618-15

28	149	11.5	107	5	PCT-US92-03993-3	Sequence 3, Appli
29	149	11.5	107	5	PCT-US95-01721-2	Sequence 2, Appli
30	148	11.4	103	1	US-08-197-795-1	Sequence 1, Appli
31	148	11.4	103	5	PCT-US95-01721-1	Sequence 1, Appli
32	146	11.2	108	2	US-08-803-899-4	Sequence 4, Appli
33	143	11.0	107	1	US-08-336-618-13	Sequence 13, Appli
34	143	11.0	107	2	US-08-963-601-1	Sequence 1, Appli
35	143	11.0	107	2	US-08-744-701-7	Sequence 7, Appli
36	143	11.0	107	3	US-08-894-173-67	Sequence 67, Appli
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38	143	11.0	107	3	US-09-398-193-67	Sequence 67, Appli
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40	143	11.0	107	4	US-08-735-848-1	Sequence 1, Appli
41	143	11.0	107	5	PCT-US92-03993-2	Sequence 2, Appli
42	143	11.0	108	1	US-07-822-966B-5	Sequence 5, Appli
43	143	11.0	108	2	US-08-803-899-3	Sequence 3, Appli
44	143	11.0	127	4	US-09-481-620A-40	Sequence 40, Appli
45	143	11.0	127	4	US-09-481-620A-72	Sequence 72, Appli

ALIGNMENTS

RESULT 1

US-09-198-452A-699  
; Sequence 699, Application US/09198452A  
; Patent No. 6559294  
; GENERAL INFORMATION:  
; APPLICANT: Grifflais, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention of infection  
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/09/198,452A  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 699  
; LENGTH: 258  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
US-09-198-452A-699

Query Match 100.0%; Score 1299; DB 4; Length 258;  
Best Local Similarity 100.0%; Pred. No. 6.3e-122;  
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNRWNLVLTVALSASCDVRSKDKDQGSILVEYKDKNDI	ELSDNQLSRITFG	60
Db	1	MNRWNLVLTVALSASCDVRSKDKDQGSILVEYKDKNDI	ELSDNQLSRITFG	60
Qy	61	HLLARQLRKSEDMFDDIAEVAKGLQAEVLVCKSA	PLTETETEYEEKMAEVQKLVPEKKSKENL	120
Db	61	HLLARQLRKSEDMFDDIAEVAKGLQAEVLVCKSA	PLTETETEYEEKMAEVQKLVPEKKSKENL	120
Qy	121	SLAEKFLKENSAGVEVQPSKQYKIIEGAGKATSGKPS	SALLHYGSGFINGOVFSSS	180
Db	121	SLAEKFLKENSAGVEVQPSKQYKIIEGAGKATSGKPS	SALLHYGSGFINGOVFSSS	180
Qy	181	EGNNEPILLPGQITPGFALCMQMGKEGTVLVYTHPDL	AYGTAGQLPNSLLIIFEINLI	240
Db	181	EGNNEPILLPGQITPGFALCMQMGKEGTVLVYTHPDL	AYGTAGQLPNSLLIIFEINLI	240
Qy	241	QASADEVAAPQEGNQGE	258	
Db	241	QASADEVAAPQEGNQGE	258	

RESULT 2

US-09-328-352-5608  
; Sequence 5608, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.

```

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5608
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5608

```

[illegible]

```

RESULT 3
US-09-762-878-4
; Sequence 4, Application US/09762878
; Patent No. 6706271
; GENERAL INFORMATION:
; APPLICANT: Thonnard, Joelle
; TITLE OF INVENTION: Cloning of BASB023 Antigen from
; TITLE OF INVENTION: Moraxella Catarrhalis
; FILE REFERENCE: BM45329
; CURRENT APPLICATION NUMBER: US/09/762,878
; CURRENT FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: PCT/EP99/05828
; PRIOR FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: GB 9817824.7
; PRIOR FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Bacteria
US-09-762-878-4

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	Query Match	22.1%	Score 287.5;	DB 4;	Length 269;
	Best Local Similarity	32.7%;	Pred. No. 1.5e-20;		
	Matches	86;	Conservative 44;	Mismatches 100;	Indels 33; Gaps 10;
QY	8	VLATVALALSVASCDVRSKDKDQGSLSVEYKNDKTINDIELSDN----	OKLSRTFFGHLL	63	
		:::::	:::::	:::::	:::::
Db	6	LVATMAATLIVGC-----	QKDTASLPKAGEKST---	VVSDKSTEIEQVSVFYGDA	55
QY	64	AROLRKSEDMFFDIAEVAK-----	GLQAELVCKSAPLTETEEVKMAE--	VOKLVFEK	114
		:::::	:::::	:::::	:::::
Db	56	GESMKKLEEN-LDIDVIKAFPGGYGVDLSALTQQTLGQAYEKKKTEEAIRQK--	QQ	112	
QY	115	KSKENLSLABKFUKENSKNAGVWVPQSPKLQYKIIEKGAGKAISCKPFSALLHYKSGFING	174		

Db	113	AAVTNKADGKFLAENAKDG-VKTPSPGLQYKVIETGTSKPTAKDGVYAAYEGR	LDG	171
Qy	175	QVPSSEGGNEPILLPGQTIPGALGQMGKGETRVLVYTHPDLAYTAGQ---	LPN	230
Db	172	TVFSSSGEAVPFM--LSQVIEGHWSEGLQLMKGGKLYLVP	QMAVYGEHGMYNAG	229
Qy	231	SLLIFFINLIQASADEVAAPQE		253
Db	230	SVLVFVIDLKKVSDKAIAAEQ		252

RESULT 4  
US-09-762-878-2  
Sequence 2, Application US/09762878  
Patent No. 6706271  
GENERAL INFORMATION:  
APPLICANT: Thonnard, Joelle  
TITLE OF INVENTION: Cloning of BASB023 Antigen from  
MORAXELLA CATARRHALIS  
FILE REFERENCE: BM45329  
CURRENT APPLICATION NUMBER: US/09/762.878  
CURRENT FILING DATE: 2001-02-14  
PRIOR APPLICATION NUMBER: PCT/EP99/05828  
PRIOR FILING DATE: 1999-08-11  
PRIOR APPLICATION NUMBER: GB 9817824.7  
PRIOR FILING DATE: 1998-08-14  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 269  
TYPE: PRT  
ORGANISM: Bacteria  
US-09-762-878-2

Query Match	21.7%	Score	282.5	DB	4	Length	269;
Best Local Similarity	32.3%	Pred. No.	4.7e-20;				
Matches	85;	Conservative	44;	Mismatches	101;	Indels	33;
Gaps	10						
Qy	8	VLATVALALSVASCDVRSKDKDQGSLVEYKONKDNDIELSDN----	QKLSRTFGHLL	63			
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Db	6	LVIATMAATLILVGC-----	QKDTASLPKAGEKST--	VWSDKSTEIEQVSYVGDA	55		
		: ::  :	::  :	:	:	:	:
Qy	64	ARQLRKSEDFPDIAEVAK-----	GLQELVCKSAPLTETEVEEKAAE--	VQKLVEEK	114		
		: ::  :	::  :	:	:	:	:
Db	56	GESMKKLEEN-LDIIDVVIKAFKGYGVDVSALTQQIQTGQA	YEKRTEEAIOKQ--	OQ	112		
		: ::  :	::  :	:	:	:	:
Qy	115	KSKENLSLABKFUKENSKNAGVVEQPSKIYKIIEKCAGAKAI	SGKPSALLHYKGSFING	174			
		: ::  :	::  :	:	:	:	:
Db	113	AAVTNKADGEKFLAENAKDG-VKTTPPGLOQYKVITEGTSKSPTAK	DGVYAAYEGRLIDG	171			
		: ::  :	::  :	:	:	:	:
Qy	175	QVSSSSGGNNPEILLPIGOTIPGFALGMCGMKEGETRVLYIH	PDLAYCTAQO---	LPBN	230		
		: ::  :	::  :	:	:	:	:
Db	172	TVPDSSSGGEAVPFM--USQVIEGWSEGLOLMKEGGKYELYVPSQ	WAYGEHGMYNAGIGN	229			
		: ::  :	::  :	:	:	:	:
Qy	231	SLLIFEINLIQASADEVAAPQE	253				
		: ::  :	::  :	:	:	:	:
Db	230	SVLVFVIDLKVKVDEKAIAAEQO	252				
		: ::  :	::  :	:	:	:	:

RESULT 5  
US-09-252-991A-17899  
; Sequence 17899, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18



QY 119 NLSLAELFKLNSKNAGVVEQPSKLYKIIKEGAGKAISSGKPSALLHYKGSFINGOVFS 178  
Db 127 NKAAGDKFTEFAAEKGVVKT-K-SGLLYLVNPGKGTFTDADRVTVNFKGMLIDKQPD 185  
QY 179 SSEGNNPILLPLGQTIPGFALGQMCKEGETRVLYIHPDLAYG---TAGQLPPNSLLIF 235  
Db 186 SSSYDRKEPLTISLKSIVPQWTEGMYKIEGGKIKLVIPPELGVQRATSG-IPANSTLVF 244  
QY 236 EINLQASADE 246  
Db 245 EVELLSVESDK 255

## RESULT 9

US-09-809-665A-143  
; Sequence 143, Application US/09809665A  
; Patent No. 6790950  
; GENERAL INFORMATION:  
; APPLICANT: Lowery E., David, et al.  
; TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions  
; FILE REFERENCE: 28341/00435  
; CURRENT APPLICATION NUMBER: US/09/809,665A  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: 60/153,453  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: 60/128,689  
; PRIOR FILING DATE: 1999-04-09  
; PRIOR APPLICATION NUMBER: 09/545,199  
; PRIOR FILING DATE: 2000-04-06  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 143  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Actinobacillus pleuropneumoniae  
US-09-809-665A-143

Query Match 17.4%; Score 226; DB 4; Length 239;  
Best Local Similarity 29.3%; Pred. No. 1.8e-14;  
Matches 60; Conservative 43; Mismatches 86; Indels 16; Gaps 5;

QY 56 SRTFGHLLARQLR-----KSEDMFFDIAEVAKGLQAEVCKSAPLTETEYEEK----- 103  
Db 34 SYAVGLMGNIQGVESQKIEPSYQDKILAGVQ-DTIKTKGLTDEDLQKLSLDY 92  
QY 104 MAEVQKLVFEKSKENLSAEKFLKNSKNAGVVEQPSKLYKIIKEGAGKAISSGKPSA 163  
Db 93 LASQESKIAAEKSKATVEAGNKRFTDYEQSGVKKT-ASGLLYKIEKAGTGSPKAEIV 151  
QY 164 LLYKGSFINGOVFSSEGNNPILLPLGQTIPGFALGQMCKEGETRVLYIHPDLAYG- 222  
Db 152 KVHYKGLTDTGTVFSDSSYDRGEPIEFQNLQIIPGWIETPMLKKGWWEIVVPPELGYGE 211  
QY 223 -TAGQLPPNSLLIFEINLIQASADE 246  
Db 212 RQAGKIPASSTLKFEIELDFKAAE 236

## RESULT 10

US-09-252-991A-21404  
; Sequence 21404, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 21404  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-21404

Query Match 16.9%; Score 219; DB 4; Length 218;  
Best Local Similarity 28.2%; Pred. No. 8e-14;  
Matches 57; Conservative 44; Mismatches 85; Indels 16; Gaps 5;

QY 50 SDNQKLSRTFGHLLARQLRS-----EDMFFDIAEVAKGLQAEVCKSAPLTETEYEE 102  
Db 21 TDEARVSYGIGRQLGDLRENVPQMTUDAVLAGLSDAFAGIDSRVSGEALSASFQVIRE 80  
QY 103 KM-AEVQKLVFEKSKENLSAEKFLKNSKNAGVVEQPSKLYKIIKEGAGKAISSGK 161  
Db 81 RMOAEAQ-----AKAEAAAGEGRAYLAENAKREGVT-VLPSSGLOFEVLSTGEGAKPSRED 134  
QY 162 SALLHYKGSFINGOVFSSEGNNPILLPLGQTIPGFALGQMCKEGETRVLYIHPDLAY 221  
Db 135 TVRTHYHGTLDGTVDSSYQYQGPAAEFPVGVIAGWVEALQLMNAGSKWRLHVPSELAY 194  
QY 222 G--TAGQLPPNSLLIFEINLIQ 241  
Db 195 GQAVGSIPPHSVLFDVELLE 216

## RESULT 11

US-09-543-681A-5818  
; Sequence 5818, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 5818  
; LENGTH: 223  
; TYPE: PRT  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-5818

Query Match 14.3%; Score 185.5; DB 4; Length 223;  
Best Local Similarity 31.2%; Pred. No. 1.9e-10;  
Matches 62; Conservative 29; Mismatches 99; Indels 9; Gaps 5;

QY 50 SDNQKLSRTFGHLLARQLRSSEDMFFDIAEVAKGLQAEV--CKSAPLTETEYEE--EKMA 105  
Db 25 STESQASYGIGLQVQCGQLTESGLQGLEPAALLAGLTDALGNTPSPVPV-ETLHNLRTWH 83  
QY 106 EVQKLVFEKSKENLSAEKFLKNSKNAGVVEQPSKLYKIIKEGAGKAISSGKPSALL 165  
Db 84 ERAEAVRQERQAALAEAGKVFLAENVKKEG-VQVTESSGLQYKVLKAGDGAIPARTDHRV 142  
QY 166 HYKGSFINGOVFSSEGNNPILLPLGQTIPGFALGQMCKEGETRVLYIHPDLAYGTAG 225  
Db 143 HYTGRLIDGTVDSSYQYQGPAAEFPVGVIAGWIEALTLMPVSGKWELIYIQLAYGERG 202  
QY 226 ---QLPPNSLLIFEINLIQ 241  
Db 203 AGAAIPPPFATLVFEVELLE 221

## RESULT 12

US-09-489-039A-8908  
; Sequence 8908, Application US/09489039A  
; Patent No. 6610836





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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 23, 2004, 12:10:54 ; Search time 191 Seconds  
(without alignments)  
777.208 Million cell updates/sec

Title: US-10-022-832-2

Perfect score: 1299

Sequence: 1 MNRWNVLATVALALSVAS.....LIQASDEVAAPQEGNQGE 258

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1299	100.0	258	1 MIP_CHLPN	Q927p3 chlamydia p
2	940	72.4	255	2 Q824R2	Q824x2 chlamydophi
3	934	71.9	255	2 Q46176	Q46176 chlamydophi
4	763	58.7	243	1 MIP_CHLTR	P26623 chlamydia t
5	733	56.4	243	1 MIP_CHLMU	Q9pjk1 chlamydia m
6	491.5	37.8	290	2 Q8WE92	Q8WE92 parachlamyd
7	491.5	37.8	290	2 CAP23107	CAP23107 parachlam
8	306	23.6	241	2 Q32827	Q32827 legionella
9	303.5	23.4	233	2 Q32836	Q32836 legionella
10	301	23.2	229	2 Q32821	Q32821 legionella
11	297	22.9	272	2 Q87YI8	Q87YI8 neisseria m
12	295.5	22.7	204	2 Q68494	Q68494 legionella
13	295.5	22.7	242	2 Q32767	Q32767 legionella
14	295	22.7	251	2 Q32768	Q32768 legionella
15	292.5	22.5	233	2 Q32749	Q32749 legionella
16	292.5	22.5	234	2 Q32844	Q32844 legionella
17	288.5	22.2	232	2 Q32763	Q32763 fluoribacte
18	288.5	22.2	232	2 Q32750	Q32750 legionella
19	288	22.2	232	2 Q6FFW0	Q6FFW0 acinetobact
20	287.5	22.1	233	2 Q32843	Q32843 legionella
21	287.5	22.1	234	2 Q32746	Q32746 legionella
22	287	22.1	235	2 Q6FFV9	Q6FFV9 acinetobact
23	287	22.1	272	2 Q87TJ0	Q87TJ0 neisseria m
24	286	22.0	249	2 Q32751	Q32751 legionella
25	284	21.9	243	2 Q79DM1	Q79DM1 legionella
26	284	21.9	249	2 Q32766	Q32766 legionella
27	284	21.9	249	2 Q32820	Q32820 legionella
28	283.5	21.8	233	2 Q79B63	Q79B63 legionella
29	283.5	21.8	257	2 Q87YB1	Q87YB1 pseudomonas
30	282.5	21.7	232	2 Q32842	Q32842 legionella
31	282.5	21.7	233	2 Q32839	Q32839 legionella

32	282	21.7	237	2	Q32762	Q32762 legionella
33	281.5	21.7	233	2	Q32838	Q32838 legionella
34	281	21.6	233	2	Q32835	Q32835 legionella
35	281	21.6	234	2	Q32759	Q32759 fluoribacte
36	281	21.6	241	2	Q32761	Q32761 legionella
37	280.5	21.5	234	2	Q32828	Q32828 legionella
38	279.5	21.5	233	2	Q32834	Q32834 legionella
39	279.5	21.5	234	2	Q32840	Q32840 legionella
40	279	21.5	238	2	Q7UKI6	Q7UKI6 rhodospirill
41	279	21.5	243	1	MIP_LEGMI	P31106 legionella
42	279	21.5	244	2	Q32825	Q32825 tatlockia m
43	278.5	21.4	233	2	Q32752	Q32752 legionella
44	278	21.4	232	2	Q32747	Q32747 legionella
45	278	21.4	233	2	Q32826	Q32826 legionella

#### ALIGNMENTS

RESULT 1  
MIP\_CHLPN  
ID MIP\_CHLPN STANDARD; PRT; 258 AA.  
AC Q927P3;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Peptidyl-prolyl cis-trans isomerase Mip precursor (EC 5.2.1.8)  
DE (PPIase) (Rotamase).  
GN Name=mip; OrderedLocusNames=CP00661, CP0066, CP00687;  
OS Chlamydia pneumoniae (Chlamydophila pneumoniae)  
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.  
OX NCBI\_TaxID=83558;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CWL029;  
RX MEDLINE=99206606; PubMed=10192388; DOI=10.1038/77116;  
RA Kalman S., Mitchell W.P., Marathe R., Lammel C.J., Fan J., Hyman R.W.,  
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;  
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";  
RL Nat. Genet. 21:385-389(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AR39;  
RX MEDLINE=20150255; PubMed=10684935;  
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,  
RA White O., Hickey E.K., Peterson J.D., Uterback T.R., Betsy K.J.,  
RA Bass S., Linher K.D., Weidman J.F., Khouri H.M., Craven B., Bowman C.,  
RA Dodson R.J., Gwinn M.L., Nelson W.C., DeSoy R.T., Kolonay J.F.,  
RA McClarty G., Salzberg S.L., Eisen J.A., Fraser C.M.;  
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";  
RL Nucleic Acids Res. 28:1397-1406(2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=J138;  
RX MEDLINE=20330349; PubMed=10871362;  
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,  
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;  
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA.";  
RL Nucleic Acids Res. 28:2311-2314(2000).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=TW-183;  
RA Geng M.M., Schummacher A., Muehldorfer I., Bensch K.W., Schaefer K.P.,  
RA Schneider S., Pohl T., Essig A., Marre R., Melchers K.;  
RT "The genome sequence of Chlamydia pneumoniae TW183 and comparison with other Chlamydia strains based on whole genome sequence analysis.";  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: PPIases accelerate the folding of proteins.  
CC -!- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline (omega=0).  
CC -!- SUBCELLULAR LOCATION: Outer membrane (By similarity).

```

CC CC -1- SIMILARITY: Belongs to the FKBP-type PPIase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; A5001648; AADI8800.1; -
CC EMBL; A5002172; AAF37972.1; -
CC EMBL; AP002547; BAA98868.1; -
CC EMBL; A5017159; AAP98616.1; -
CC PIR; B86573; B86573.
CC PIR; F72052; F72052.
CC HSSP; Q13451; 1KT0.
CC TIGR; CP0086; -.
CC InterPro; IPR000774; FKBP Nterm.
CC InterPro; IPR001179; FKBP_PPIase.
CC Pfam; PF00254; FKBP_C; 1.
CC Pfam; PF01346; FKBP_N; 1.
CC ProDom; PD001516; FKBP_Nterm; 1.
CC PROSITE; PS00059; FKBP_PPIase; 1.
CC PROSITE; PS00013; PROKAR LIPOPROTEIN; UNKNOWN 1.
CC Complete proteome; Isomerase; Outer membrane; Rotamase; Signal.
FT SIGNAL 1 15 Potential.
FT CHAIN 16 258 Peptidyl-prolyl cis-trans isomerase Mip.
FT DOMAIN 160 243 PPIase, FKBP-type.
SQ SEQUENCE 258 AA; 28330 MW; 65E3CE4EAC022552 CRC64;

Query Match 100.0%; Score 1299; DB 1; Length 258;
Best Local Similarity 100.0%; Pred. No. 4.9e-82;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRRLNLVLTVALSVASCDVRSKDKDKQGSLSVEYKDKNDTNDIELSDNQLKSRFTG 60
DB 1 MNRRLNLVLTVALSVASCDVRSKDKDKQGSLSVEYKDKNDTNDIELSDNQLKSRFTG 60
QY 61 HLLARQLRKSEDMFFDIAEVAKGLQAEVLCKAPLTETEYEKMAEVLKVFEEKSKENL 120
DB 61 HLLARQLRKSEDMFFDIAEVAKGLQAEVLCKAPLTETEYEKMAEVLKVFEEKSKENL 120
QY 121 SLAEKFLKSNKAGVVEVQPSKLYKIKEGAGKAIKSGKPSALLHYKGSFINGQVFSSS 180
DB 121 SLAEKFLKSNKAGVVEVQPSKLYKIKEGAGKAIKSGKPSALLHYKGSFINGQVFSSS 180
QY 181 EGNNEPILLPLGOTIPGFALGMQGMKEGTRVLYIHDPDAYGTAGQLPPNSLLIFEINLI 240
DB 181 EGNNEPILLPLGOTIPGFALGMQGMKEGTRVLYIHDPDAYGTAGQLPPNSLLIFEINLI 240
QY 241 QASADEVAAPQSGNOGE 258
DB 241 QASADEVAAPQSGNOGE 258

RESULT 2
Q824R2 PRELIMINARY; PRT; 255 AA.
ID Q824R2
AC Q824R2
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Peptidyl-prolyl cis-trans isomerase Mip.
GN Name:mip; OrderedLocName:CCAA00078;
OS Chlamydomophila caviae.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomophila.
OX NCBI_TaxID=83557;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GPIC;
RX MEDLINE=22569155; PubMed=12682364;
RA Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,

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RA Heidelberg J.F., Holtzapfel E.K., Khouri H.M., Federova N.B.,
RA Carty H.A., Unayam L.A., Haft D.H., Peterson J.D., Beanan M.J.,
RA White O., Salzberg S.L., Hsia R.-C., McCarthy G., Rank R.G.,
RA Bavoil P.M., Fraser C.M.;
RT "Genome sequence of Chlamydomophila caviae (Chlamydia psittaci GPIC):
RT examining the role of niche-specific genes in the evolution of the
RT Chlamydiaceae.";
RL Nucleic Acids Res. 31:2134-2147(2003).
CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
CC (omega=0).
CC -1- SIMILARITY: Belongs to the FKBP-type PPIase family.
CC EMBL; A5016994; AAP04830.1; -.
CC HSSP; P20380; 1FD9.
CC TIGR; CCA00078; -.
CC GO; GO:001855; P:isomerase activity; IEA.
CC GO; GO:008457; P:protein folding; IEA.
CC InterPro; IPR000774; FKBP_Nterm.
CC InterPro; IPR001179; FKBP_PPIase.
CC Pfam; PF00254; FKBP_C; 1.
CC Pfam; PF01346; FKBP_N; 1.
CC ProDom; PD001516; FKBP_Nterm; 1.
CC PROSITE; PS00059; FKBP_PPIase; 1.
CC PROSITE; PS00013; PROKAR LIPOPROTEIN; UNKNOWN 1.
CC Complete proteome; Isomerase; Rotamase.
SQ SEQUENCE 255 AA; 28195 MW; 84FD9C3E88BB61DF CRC64;

Query Match 72.4%; Score 940; DB 2; Length 255;
Best Local Similarity 72.7%; Pred. No. 3.5e-57;
Matches 181; Conservative 34; Mismatches 30; Indels 4; Gaps 1;

QY 1 MNRRLNLVLTVALSVASCDVRSKDKDKQGSLSVEYKDKNDTNDIELSDNQLKSRFTG 60
DB 1 MKKRHLMTITVVSFSIASCDSSSQRGNQ-----IAQVEEKSANDSLSVNOQISRTFG 56
QY 61 HLLARQLRKSEDMFFDIAEVAKGLQAEVLCKAPLTETEYEKMAEVLKVFEEKSKENL 120
DB 57 HLLARQLRKSEDMFFDIAEVAKGLQAEVLCKAPLTETEYEKMAEVLKVFEEKSKENL 116
QY 121 SLAEKFLKSNKAGVVEVQPSKLYKIKEGAGKAIKSGKPSALLHYKGSFINGQVFSSS 180
DB 117 SLAEKFLKSNKAGVVEVQPSKLYKIKEGAGKAIKSGKPSALLHYKGSFINGQVFSSS 176
QY 181 EGNNEPILLPLGOTIPGFALGMQGMKEGTRVLYIHDPDAYGTAGQLPPNSLLIFEINLI 240
DB 177 EANKPEILLPLAQTIPGFALGMQGMKEGTRVLYIHDPDAYGTAGQLPPNSLLIFEINLI 236
QY 241 QASADEVA 249
DB 237 ETDDSVAA 245

RESULT 3
Q46176 PRELIMINARY; PRT; 255 AA.
ID Q46176
AC Q46176
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mip protein.
GN Name:mip;
OS Chlamydomophila caviae.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomophila.
OX NCBI_TaxID=83557;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GPIC;
RX MEDLINE=97090413; PubMed=8936321;
RA Rockey D.D., Chesebro B.B., Heinzen R.A., Hackstadt T.;
RT "A 28 kDa major immunogen of Chlamydia psittaci shares identity with
RT Mip proteins of Legionella spp. and Chlamydia trachomatis-cloning and
RT characterization of the C. psittaci mip-like gene.";
RL Microbiology 142:945-953(1996).
CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
CC (omega=0).

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CC -!- SIMILARITY: Belongs to the FKBP-type PPIase family.
DR EMBL; L39892; AAB41346.1; -.
DR HSP; F20380; IFD9.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR000774; FKBP_Nterm.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00254; FKBP_C; 1.
DR Pfam; PF01346; FKBP_N; 1.
DR ProDom; PD001516; FKBP_Nterm; 1.
DR PROSITE; PS50059; FKBP_PPIASE_3; 1.
KW Isomerase; Rotamase.
SQ SEQUENCE 255 AA; 828271 MW; 8950F9F1E61961DF CRC64;

Query Match 71.9%; Score 934; DB 2; Length 255;
Best Local Similarity 72.3%; Pred. No. 9.2e-57;
Matches 180; Conservative 34; Mismatches 31; Indels 4; Gaps 1;

QY 1 MNRRLNLVATVALASVASCDSVRSKDKDGSLVEYKDKNTDNDIELSDNKLRTFTG 60
DB 1 MKRWHLMIITVVSFSTASCDSSSQGNQ-----IAQVEKSAANDSOLSVNQQLSRTFG 56

QY 61 HLLARQLRKSEDMFFDIAEAVAKGLQAEVLCKSAPLTETETEYEEKMAEVQKLVFEKKSKENL 120
DB 57 HLLARQLAKSEDIWMIDIAEAVAKGLQAEVLCKSAPLTETETEYEEKMAEIQKLVFEKKAKENL 116

QY 121 SLAEKFLKSNKAGVVEQVPSKLYKIIEKGAGKAIKSGKPSALLHYKGSFINGQVFS 180
DB 117 YLAERFLOENKNSGVVEQVADKLYRIYKVGEGTGRAISGKPSALLHYKGTFTDGGVFS 176

QY 181 EGNNEPILLPGOTIPGALGQMGKEGTRVLVYTHPDLAYCTAGQLPPNSLLIFEINLI 240
DB 177 EANKPILLPLLAQTIPGALGQMGKEGTRILYIHPDLAYCTAGQLPPNSLLIFEINLI 236

QY 241 QASADEVAA 249
DB 237 ETTDSVAA 245

RESULT 4
MIP_CHLTR
ID MIP_CHLTR STANDARD; PRT; 243 AA.
AC
DT 01-AUG-1992 (Rel. 23, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Peptidyl-prolyl cis-trans isomerase Mip precursor (EC 5.2.1.8)
DE (PPIase) (Rotamase) (27 kDa membrane protein) (Chl-Mip).
GN Name=mip; OrderedLocustNames=CT541;
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Serovar B, Serovar E, and Serovar L2;
RX MEDLINE=93023883; PubMed=1406289;
RA Lundemose A.G., Rouch D.A., Birkelund S., Christiansen G.,
RT Pearce J.H.;
RA "Chlamydia trachomatis Mip-like protein.";
RL Mol. Microbiol. 6:2539-2548(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=D/OW-3/Cx;
RX MEDLINE=9900809; PubMed=9784136;
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.I., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis.";
RL Science 282:754-759(1998).
RN [3]
RP SEQUENCE OF 69-243 FROM N.A.
RC STRAIN=Serovar L2;
RX MEDLINE=91194539; PubMed=2013997;

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RA RA
RA Christian Hansen G.;
RA "Chlamydia trachomatis contains a protein similar to the Legionella
RA pneumophila mip gene product.";
RL Mol. Microbiol. 5:109-115(1991).
CC -!- FUNCTION: PPIases accelerate the folding of proteins.
CC -!- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
CC (omega=0).
CC -!- SUBCELLULAR LOCATION: Outer membrane.
CC -!- SIMILARITY: Belongs to the FKBP-type PPIase family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC
DR EMBL; X66126; CAA46917.1; -.
DR EMBL; X66127; CAA46918.1; -.
DR EMBL; X66128; CAA46919.1; -.
DR EMBL; AE001324; AAC68143.1; -.
DR PIR; S25255; S25255.
DR PIR; S28638; S28638.
DR HSP; P18203; 1FKL.
DR PHCI-2DPAGE; P26623; -.
DR Signa-2DPAGE; P26623; -.
DR InterPro; IPR000774; FKBP_Nterm.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00254; FKBP_C; 1.
DR Pfam; PF01346; FKBP_N; 1.
DR ProDom; PD001516; FKBP_Nterm; 1.
DR PROSITE; PS50059; FKBP_PPIASE; 1.
KW Complete proteome; Isomerase; Outer membrane; Rotamase; Signal.
FT SIGNAL 1 14
FT CHAIN 15 243
FT DOMAIN 152 235
FT VARIANT 56 56 S -> A (in serovar L2).
FT VARIANT 117 117 K -> E (in serovar L2).
FT CONFLICT 137 138 QY -> HD (in Ref. 3).
SQ SEQUENCE 243 AA; 26663 MW; 677F9D551A95A382 CRC64;

Query Match 58.7%; Score 763; DB 1; Length 243;
Best Local Similarity 61.1%; Pred. No. 6e-45;
Matches 149; Conservative 36; Mismatches 49; Indels 10; Gaps 2;

QY 5 WNLVLTATVALASVASCDSVRSKDKDGSLVEYKDKNTDNDIELSDNKLRTFTGHLLA 64
DB 7 WLMF---AVALPIVGC-----DNGGGSQTSATEKSMVEDSALTDNKLRTFTGHLLS 56

QY 65 RQLRKSEDMFFDIAEAVAKGLQAEVLCKSAPLTETETEYEEKMAEVQKLVFEKKSKENLSLAE 124
DB 57 RQLRTEDEFSLDLVEVINGMQSEIDGQSAPLTETETEYEQMAEVQKASFEAKCSENLSAE 116

QY 125 KFLKSNKAGVVEQVPSKLYKIIEKGAGKAIKSGKPSALLHYKGSFINGQVFSSEGN 184
DB 117 KFLKENKEKAGVIELEPNKLYRVVVEGTGRVLSGKPTALLHYTGSFIDGKVPDSEK 176

QY 185 EPILLPGOTIPGALGQMGKEGTRVLVYTHPDLAYCTAGQLPPNSLLIFEINLIQASA 244
DB 177 EPILLPLTKVIPGFSQGNQMGKEGTRVLVYTHPDLAYCTAGQLPPNSLLIFEVKLEAND 236

QY 245 DEVA 248
DB 237 DNVS 240

RESULT 5
MIP_CHLMU
ID MIP_CHLMU STANDARD; PRT; 243 AA.
AC Q9FKI;
DT 16-OCT-2001 (Rel. 40, Created)

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DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 01-OCT-2004 (Rel. 45, Last annotation update)
DE Peptidyl-prolyl cis-trans isomerase Mip precursor (EC 5.2.1.8)
DE (PPIase) (Rotamase).
GN Name:mip; OrderedLocusNames=TC0828;
OS Chlamydia muridarum.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OC NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MoPn / Nigg;
RC MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J.D., Utterback T.R., Berry K.J.,
RA Bass S., Linher K.D., Weidman J.F., Khouri H.M., Craven B., Bowman C.,
RA Dodson R.J., Gwinn M.L., Nelson W.C., DeBoy R.T., Kolonay J.F.,
RA McClarty G., Salzberg S.L., Eisen J.A., Fraser C.M.;
RA "genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
CC -1- FUNCTION: PPIases accelerate the folding of proteins.
CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
CC (omega=0).
CC -1- SUBCELLULAR LOCATION: Outer membrane (By similarity).
CC -1- SIMILARITY: Belongs to the FKBP-type PPIase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@sb-sib.ch).
CC -----
DR EMBL; AE002349; AAF39628.1; ALT_INIT.
DR HSP; P27124; 1ROT.
DR TIGR; TC0828; -.
DR InterPro; IPR000774; FKBP_Nterm.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00254; FKBP_C; 1.
DR Pfam; PF01346; FKBP_N; 1.
DR ProDom; PD001516; FKBP_Nterm; 1.
DR PROSITE; PS00059; FKBP_PPIASE; 1.
DR Complete proteome; Isomerase; Outer membrane; Rotamase; Signal.
KW SIGNAL
FT SIGNAL 1 14 Potential.
FT CHAIN 15 243 Peptidyl-prolyl cis-trans isomerase Mip.
FT DOMAIN 152 235 PPIase, FKBP-type.
FT DOMAIN 243 AA; 26781 MW; 4556004B7511A72C CRC64;
SQ SEQUENCE
Query Match 56.4%; Score 733; DB 1; Length 243;
Best Local Similarity 59.4%; Pred. No. 7.2e-43;
Matches 145; Conservative 35; Mismatches 54; Indels 10; Gaps 2;
QY 5 WNLVATVALALSVASCDVRSKDKQGSILVEYKDNKNDTNDIELSDNQKLSRTFGHLLA 64
DB 7 WMLNF---AVALPILGC-----DNNGSQTSANGKDWEDSVLTQKLSRTFGHLLA 56
QY 65 RQLRKSDEMFPIAEVAGLQAEVLVCKSAPIETETEYEEKMAEVQKLVPEKSKENLSLAE 124
DB 57 RQLSSTEDFTLDLTEVIKGMQSETEGKSAPLTDSEYETQMALVQKSAPEKSCSENLSAE 116
QY 125 KFLKENSKNAGVEVQPSKLOYKIIKEGAGKAI SGKPSALHYKGSFTINGOVFSSSGNN 184
DB 117 KFLKENDKGEVIELEPNKLYRIVKEGTGRVLTGKPNALLHYTGSPFNGKVFDTSEK 176
QY 185 EPILLPLGQITPGFALGMQGMKEGETRVLVYHPDLAYGTACQLPPNSLLIPEINLIQASA 244
DB 177 DPILLPLTKVLSGFSQGMQGNREGEVRVLYIHPDLAYGTSQQLPPNSLLIEVKLIAND 236
QY 245 DEVA 248
DB :337 DNVS 240

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RA Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,  
RA Fartmann B., Brandt P., Nyakatura G.J., Droege M., Frishman D.,  
RA Rattai T., Mewes H., Wagner M.;  
RT "Genome sequence of an amoeba symbiont and its use for reconstructing  
the evolutionary history of chlamydiae.";  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=UW825;  
RA Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,  
RA Fartmann B., Brandt P., Nyakatura G.J., Droege M., Frishman D.,  
RA Rattai T., Mewes H., Wagner M.;  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX908798; CAP23107.1; -;  
KW Isomerase.  
SQ SEQUENCE 290 AA; 31682 MW; 1993E60549FE0B7E CRC64;  
Query Match 37.8%; Score 491.5; DB 2; Length 290;  
Best Local Similarity 49.0%; Pred. No. 4.7e-26;  
Matches 96; Conservative 35; Mismatches 64; Indels 1; Gaps 1;  
QY 51 DNQKLSRTFGHLLARQLRKSEDMFFDIAEVAQGLQAEVLVCKSAPLTETETEYEEKMAEVQKL 110  
DB 51 DMQKLSAEAFGFIENL-QAPGLQFDLEAIKIGREGAAGKPAPLSEKEYEEMMAVQER 109  
QY 111 VFEKSKENLSLAEKFLKENSKNAGVVEVQPSKLYKIIKEGAGKAIISGKPSALLHYKGS 170  
DB 110 AFKEMSTKLNKANDFMKNSQSTDTVEIPGKLYSVEKEGTGPVPEPHSPKHYTGK 169  
QY 171 FINGOVSSSEGNNEPILLPGQTTPGALGMOGKEGTRVLYIHPDLAYGTAGOLPPN 230  
DB 170 YQDGFVFTSEMDGFIITPLDQTPGFSKGVGMKEGKRRLYVHPDLGYGTGQLPPN 229  
QY 231 SLLEIFENLIOASDE 246  
DB 230 ELLIFDIEIVKANSDD 245  
RESULT 8  
O32827 PRELIMINARY; PRT; 241 AA.  
AC O32827;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Macrophage infectivity potentiator.  
CN Name=mip;  
OS Legionella nautilum.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;  
OC Legionellaceae; Legionella.  
OX NCBI\_TaxID=45070;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 49506;  
RX MEDLINE=98010353; PubMed=9350870;  
RA Ratcliff R.M., Donnellan S.C., Lanser J.A., Manning P.A.,  
RA Heuzenroeder M.W.;  
RT "Interspecies sequence differences in the Mip protein from the genus  
Legionella; implications for function and evolutionary relatedness.";  
RL Mol. Microbiol. 25:1149-1158(1997).  
CC -!- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline  
(omega=0).  
CC [1]  
CC -!- SIMILARITY: Belongs to the FKBP-type PPIase family.  
DR EMBL; U22133; AAC45699.1; -;  
DR HSSP; P20380; 1FD9.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0003755; F:peptidyl-prolyl cis-trans isomerase activity; IEA.  
DR GO; GO:0006457; P:protein folding; IEA.  
RA Heuzenroeder M.W.;  
RT "Interspecies sequence differences in the Mip protein from the genus  
Legionella; implications for function and evolutionary relatedness.";  
RL Mol. Microbiol. 25:1149-1158(1997).  
CC -!- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline  
(omega=0).  
CC [1]  
CC -!- SIMILARITY: Belongs to the FKBP-type PPIase family.  
DR EMBL; U22133; AAC45699.1; -;  
DR HSSP; P20380; 1FD9.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0003755; F:peptidyl-prolyl cis-trans isomerase activity; IEA.  
DR GO; GO:0006457; P:protein folding; IEA.  
DR InterPro; IPR000774; FKBP Nterm.  
DR InterPro; IPR001179; FKBP PPIase.  
DR InterPro; IPR008104; INFPNTIATR.  
DR Pfam; PF00254; FKBP\_C; 1.  
DR Pfam; PF01346; FKBP\_N; 1.  
CC -!- SIMILARITY: Belongs to the FKBP-type PPIase family.  
DR EMBL; U22133; AAC45699.1; -;  
DR HSSP; P20380; 1FD9.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0003755; F:peptidyl-prolyl cis-trans isomerase activity; IEA.  
DR GO; GO:0006457; P:protein folding; IEA.  
DR InterPro; IPR000774; FKBP Nterm.  
DR InterPro; IPR001179; FKBP PPIase.  
DR InterPro; IPR008104; INFPNTIATR.  
DR Pfam; PF00254; FKBP\_C; 1.  
DR Pfam; PF01346; FKBP\_N; 1.

DR PRINTS; PR01730; INFPNTIATR.  
DR ProDom; PD001516; FKBP\_Nterm; 1.  
DR PROSITE; PS50059; FKBP\_PPIASE\_3; 1.  
KW Isomerase; Rotamase.  
SQ SEQUENCE 241 AA; 25788 MW; 2C36P75ABEAD9E93 CRC64;  
Query Match 23.6%; Score 306; DB 2; Length 241;  
Best Local Similarity 38.8%; Pred. No. 2.7e-13;  
Matches 78; Conservative 31; Mismatches 80; Indels 12; Gaps 4;  
QY 50 SDNQKLSRTFGHLLARQLRKSEDMFFDIAEVAQGLQAEVLVCKSAPLTETETEYEEKMAEVQK 109  
DB 50 TDTDKLSYSICADLGKPKK-QGIDISPAAMAKGLQDMSGGQLLLTSEQMKVNLKFKQK 94  
QY 110 LV-----FEKSKENLSLAEKFLKENSKNAGVVEVQPSKLYKIIKEGAGKAIISGKPS 162  
DB 95 ELMKRSAEFNKSEENKSGEAFLEKONKSKDGVVSL-PSGLQVLYKILEKGDCAKPAKDDT 153  
QY 163 ALLHYKGSFINGOVSSSEGNNEPILLPGQTTPGALGMOGKEGTRVLYIHPDLAYG 222  
DB 154 VTVEYTGRLINGQVDFDSTETGKPAATFKVSVQIPGWTEALQMPGSGSTWETVIPSCLAYG 213  
QY 223 --TAGQLPPNSLLIFEINLI 240  
DB 214 PRSVGGPIGPNETLIFKHLI 234  
RESULT 9  
O32836 PRELIMINARY; PRT; 233 AA.  
ID O32836  
AC O32836;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Macrophage infectivity potentiator.  
CN Name=mip;  
OS Legionella quinilivani.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;  
OC Legionellaceae; Legionella.  
OX NCBI\_TaxID=45073;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 43830;  
RX MEDLINE=98010353; PubMed=9350870;  
RA Ratcliff R.M., Donnellan S.C., Lanser J.A., Manning P.A.,  
RA Heuzenroeder M.W.;  
RT "Interspecies sequence differences in the Mip protein from the genus  
Legionella; implications for function and evolutionary relatedness.";  
RL Mol. Microbiol. 25:1149-1158(1997).  
CC -!- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline  
(omega=0).  
CC [1]  
CC -!- SIMILARITY: Belongs to the FKBP-type PPIase family.  
DR EMBL; U2217; AAC45703.1; -;  
DR HSSP; P20380; 1FD9.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0003755; F:peptidyl-prolyl cis-trans isomerase activity; IEA.  
DR GO; GO:0006457; P:protein folding; IEA.  
DR InterPro; IPR000774; FKBP Nterm.  
DR InterPro; IPR001179; FKBP PPIase.  
DR InterPro; IPR008104; INFPNTIATR.  
DR Pfam; PF00254; FKBP\_C; 1.  
DR Pfam; PF01346; FKBP\_N; 1.  
DR PRINTS; PR01730; INFPNTIATR.  
DR ProDom; PD001516; FKBP\_Nterm; 1.  
DR PROSITE; PS50059; FKBP\_PPIASE\_3; 1.  
KW Isomerase; Rotamase.  
SQ SEQUENCE 233 AA; 24934 MW; 7P5E61B25249DC16 CRC64;  
Query Match 23.4%; Score 303.5; DB 2; Length 233;  
Best Local Similarity 33.9%; Pred. No. 3.8e-13;  
Matches 85; Conservative 42; Mismatches 87; Indels 37; Gaps 7;  
QY 10 ATVALALSVCDSVRSKDKDQGSLSVYKONKOTNDIELS-DNQKLSRTFGHLLARQLR 68





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Db 120 HKADAKANKKEGEAFLENAADKG-VKTTASGLQYKTKQEGSKQPTKDDIVTVEYEGRL 178
Qy 172 INGQVFSSEGNBPILLPLGQTIIPGALGMQMGKEGTRVLYIHPDLAY---GTAGQLP 228
Db 179 IDGTVFDSKANGGVPVTFPLSQVPGWTEGVOLLKEGGEATFYIPSNLAYREQGANGKIG 238
Qy 229 PMSLIFINLIQASADVAAPVQ 252
Db 239 FNATLVFDVKLVKIGAPENAPAK 262

RESULT 12
ID O68494 PRELIMINARY; PRT; 204 AA.
AC O68494;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Macrophage infectivity potentiator protein (fragment).
GN Name=mip;
OS Legionella sp. L.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=74303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LC1863;
RX MEDLINE=98281687; PubMed=9620377;
RA Ratcliff R.M., Lanser J.A., Manning P.A., Heuzenroeder M.W.;
RT "Sequence-based classification scheme for the genus Legionella
targeting the mip gene.";
RL J. Clin. Microbiol. 36:1560-1567(1998).
CC -!- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
(omega=0).
CC -!- SIMILARITY: Belongs to the FKBP-type PPIase family.
DR EMBL; AF047754; AAC08978.1; -.
DR HSSP; P20380; 1FD9.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0003755; P:peptidyl-prolyl cis-trans isomerase activity; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR000774; FKBP_Nterm.
DR InterPro; IPR001179; FKBP_PPIase.
DR Pfam; PF00254; FKBP_C; 1.
DR PRINTS; PR01730; INFOTNTIATR.
DR ProDom; PD001516; FKBP_Nterm; 1.
DR PROSITE; PS50059; FKBP_PPIASE_3; 1.
KW Isomerase; Rotamase.
FT NON_TER 1
FT NON_TER 204
SQ SEQUENCE 204 AA; 22279 MW; 4E87F5B3A2CF6889 CRC64;

Query Match 22.7%; Score 295.5; DB 2; Length 204;
Best Local Similarity 34.9%; Pred. No. 1.2e-12;
Matches 76; Conservative 34; Mismatches 77; Indels 31; Gaps 4;

Qy 12 VALALSVASCDVRKDKDQGSILVEYKDKNTDIELSDNKLRTFGHLLARQIKSE 71
Db 7 LAMTITVTAATDQSLKNDKD-----KLSYSTGIDIGKRNFRK-Q 43
Qy 72 DMFFDIAEVAKGLQAEVLCKSAPLTETEYEEKMAEVQKLV-----PEKSKENLSLAE 124
Db 44 GLEVNPVLAKGNQGLSGSKQLLIDEQKVELSNFQSKLMAKRTAEFNKKAENKQKE 103
Qy 125 KFLKENSKNAGVVEQPSKLYKIIKEGAGKAISGKPSALLHYKGSFINGQVFSSEGN 184
Db 104 AFLKENSKEGVVAL-PSGLQYKIIKEGAGKAISGKPSALLHYKGSFINGQVFSSEGN 184
Qy 185 EPILLPLGQTIIPGALGMQMGKEGTRVLYIHPDLAYG 222
Db 163 KPATFKLSQVIRPGWTEALQLMPEGSTWIIYVPSDLAYG 200
```

```
RESULT 13
ID O32767 PRELIMINARY; PRT; 242 AA.
AC O32767;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Macrophage infectivity potentiator.
GN Name=mip;
OS Legionella israelensis;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 43119;
RX MEDLINE=98010353; PubMed=9350870;
RA Ratcliff R.M., Donnellan S.C., Lanser J.A., Manning P.A.,
Heuzenroeder M.W.;
RT "Interspecies sequence differences in the Mip protein from the genus
Legionella; implications for function and evolutionary relatedness.";
RL Mol. Microbiol. 25:1149-1158(1997).
CC -!- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
(omega=0).
CC -!- SIMILARITY: Belongs to the FKBP-type PPIase family.
DR EMBL; U92208; AAC45692.1; -.
DR HSSP; P20380; 1FD9.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0003755; P:peptidyl-prolyl cis-trans isomerase activity; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR000774; FKBP_PPIase.
DR InterPro; IPR001179; FKBP_PPIase.
DR InterPro; IPR008104; INFOTNTIATR.
DR Pfam; PF00254; FKBP_C; 1.
DR Pfam; PF01346; FKBP_N; 1.
DR PRINTS; PR01730; INFOTNTIATR.
DR ProDom; PD001516; FKBP_Nterm; 1.
DR PROSITE; PS50059; FKBP_PPIASE_3; 1.
KW Isomerase; Rotamase.
SQ SEQUENCE 242 AA; 26162 MW; 7B6ADF85B67ABBCD CRC64;

Query Match 22.7%; Score 295.5; DB 2; Length 242;
Best Local Similarity 31.6%; Pred. No. 1.4e-12;
Matches 80; Conservative 44; Mismatches 92; Indels 37; Gaps 6;

Qy 7 LVLATV---ALALSVASCDVRKDKDQGSILVEYKDKNTDIELSDNKLRTFGHLL 63
Db 5 LVAATVMSMAISTAATAATDASSLN-----TDVEKLUSYSIGADL 42
Qy 64 ARQLRKSDMFFDIAEVAKGLQAEVLCKSAPLTE-----TEYEEKMAEVQKLVPEKKS 116
Db 43 GKNFKK-OGIETDPOAMAAGKDGSGDKLKLTEQOMRDVLNKFQELMAKENAFNKKA 101
Qy 117 KENLSLAEKFLKENSKNAGVVEQPSKLYKIIKEGAGKAISGKPSALLHYKGSFINGQV 176
Db 102 AENKAKGEAFLEQNKKEGVTL-PSGLQYKIIKEGAGTGTGKPSKSDTVTVETGRLINGQV 160
Qy 177 FSSSEGNNEPILLPLGQTIIPGALGMQMGKEGTRVLYIHPDLAYG---TAQLPNSLL 233
Db 161 FDSSEVRGKPTAFKVSQVIRPGWTEALQMLPAGSTWIIYVPSDLAYGPRISGPIGNETL 220
Qy 234 IFEINLIQASDE 246
Db 221 IFKIHLISVKDK 233

RESULT 14
ID O32768 PRELIMINARY; PRT; 251 AA.
AC O32768;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
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DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Macrophage infectivity potentiator.
GN Name=mip;
OS Legionella jordanis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=456;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33263;
RX MEDLINE=98010353; PubMed=9350870;
RA Ratcliff R.M., Donnellan S.C., Lanser J.A., Manning P.A.,
RA Heuzenroeder M.W.;
RT "Interspecies sequence differences in the Mip protein from the genus
RT Legionella; implications for function and evolutionary relatedness.";
RL Mol. Microbiol. 25:1149-1158 (1997).
CC -|- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
CC (omega=0).
CC -|- SIMILARITY: Belongs to the FKBP-type PPIase family.
DR EMBL; U92209; AAC45693.1; -
DR HSSP; P20380; 1FD9.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0003755; F:peptidyl-prolyl cis-trans isomerase activity; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR000774; FKBP_Nterm.
DR InterPro; IPR001179; FKBP_PPIase.
DR InterPro; IPR008104; INFOTNTIATR.
DR Pfam; PF00254; FKBP_C; 1.
DR Pfam; PF01346; FKBP_N; 1.
DR PRINTS; PR01730; INFOTNTIATR.
DR PRODOM; PD001516; FKBP_Nterm; 1.
DR PROSITE; PS50059; FKBP_PPIASE_3; 1.
KW Isomerase; Rotamase.
SQ SEQUENCE 251 AA; 26681 MW; EAE0386659994331 CRC64;

Query Match 22.7%; Score 295; DB 2; Length 251;
Best Local Similarity 33.5%; Pred. No. 1.6e-12;
Matches 86; Conservative 39; Mismatches 110; Indels 22; Gaps 7;

OY 4 RNVLVLTAV---ALALSVASCDVRSKDKDQGSILVEYKDKNDTNDIEL-SDNQKLSRTF 59
DB 2 KMLRLVAAVNGLAWTGAIAANDATNTATSPAS-----NTATSTATSLNSDMDKLSYSI 55
OY 60 GHLLARQLRKSDFDIAEVAKQLAELVCKSAPLTETETEYEEKMAEVOK-----LVF 112
DB 56 GADLGNFKK-QGIDINPAAMAKGLQDGMSSQLMTEQMKVLDNFKQDLMAKRNAEF 114
OY 113 EKSKENLSLAEKFLKENSKNAGVVEVQPSKLYKIKKGAGKAIKSKPSALLHYKGSFI 172
DB 115 SKKADENKSKGEAFNANKSKEGVWSL-PSGLQYKILEKNGVKPSKDDTIVTEYTGKLI 173
OY 173 NGOVSSSSGNNEPILLPLGQTIPGFALGQMGKEGTRVLYIHPDLAYG---TAGQLPP 229
DB 174 DGQVFDSTERTGTPATFKVSVQVIFGWTALQMLPAGSTWEIYIPSLAYGPRSVGGPIGP 233
OY 230 NSLLIFEINLIQASADE 246
DB 234 NETLIFKIHLSVKKSD 250

RESULT 15
O32749
ID O32749 PRELIMINARY; PRT; 233 AA.
AC O32749;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Macrophage infectivity potentiator.
GN Name=mip;
OS Legionella birminghamensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.

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OX NCBI_TaxID=28083;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 43702;
RX MEDLINE=98010353; PubMed=9350870;
RA Ratcliff R.M., Donnellan S.C., Lanser J.A., Manning P.A.,
RA Heuzenroeder M.W.;
RT "Interspecies sequence differences in the Mip protein from the genus
RT Legionella; implications for function and evolutionary relatedness.";
RL Mol. Microbiol. 25:1149-1158 (1997).
CC -|- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
CC (omega=0).
CC -|- SIMILARITY: Belongs to the FKBP-type PPIase family.
DR EMBL; U91608; AAC45670.1; -
DR HSSP; P20380; 1FD9.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0003755; F:peptidyl-prolyl cis-trans isomerase activity; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR000774; FKBP_Nterm.
DR InterPro; IPR001179; FKBP_PPIase.
DR InterPro; IPR008104; INFOTNTIATR.
DR Pfam; PF00254; FKBP_C; 1.
DR Pfam; PF01346; FKBP_N; 1.
DR PRINTS; PR01730; INFOTNTIATR.
DR PRODOM; PD001516; FKBP_Nterm; 1.
DR PROSITE; PS50059; FKBP_PPIASE_3; 1.
KW Isomerase; Rotamase.
SQ SEQUENCE 233 AA; 24877 MW; 0297C61D08C41A32 CRC64;

Query Match 22.5%; Score 292.5; DB 2; Length 233;
Best Local Similarity 33.9%; Pred. No. 2.2e-12;
Matches 82; Conservative 36; Mismatches 89; Indels 35; Gaps 6;

OY 10 ATVALALSVASCDVRSKDKDQGSILVEYKDKNDTNDIELS-DNOKLSRTFGHLLARQLR 68
DB 9 ATMGLAMSTATA-----ASDVTLSMDKLSYSGADLGNFK 46
OY 69 KSEDMDFFDIAEVAKQLAELVCKSAPLTETETEYEEKMAEVOK-----LVFEKSKENLS 121
DB 47 K-QGTEINPTAMAKGLQDGMSSQLMTEQMKVLDNFKQDLMAKRNAEFSKSEENKA 105
OY 122 LAEKFLKENSKNAGVVEVQPSKLYKIKKGAGKAIKSKPSALLHYKGSFINGQVFSSE 181
DB 106 KGTEFLSQNKSEGVWSL-PSGLQYKIKIETSGAKPAKDDTIVTEYTGRTIDQVFDSTD 164
OY 182 GNNEPILLPLGQTIPGFALGQMGKEGTRVLYIHPDLAYG---TAGQLPNSLLIFEIN 238
DB 165 KSGKPATFKVSVQVIFGWTALQMLPAGSTWEIYIPSLAYGPRSVGGPIGPNETLIFKIH 224
OY 239 LI 240
DB 225 LI 226

Search completed: November 23, 2004, 12:18:24
Job time : 193 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: November 23, 2004, 12:10:53 ; Search time 40 Seconds  
(without alignments)  
620.598 Million cell updates/sec

Title: US-10-022-832-2  
Perfect score: 1299  
Sequence: 1 MNRRLNLVATVALSASV.....LIQASDAEVAAPQEGNQGE 258

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1299	100.0	258	2 F72052	peptidyl-prolyl ci
2	1299	100.0	258	2 B86573	fkbp-type peptidyl
3	763	58.7	243	2 S28638	probable fkbp-type
4	762	58.7	243	2 S25255	mip-like protein p
5	733	56.4	261	2 D81660	peptidyl-prolyl ci
6	297	22.9	272	2 C81068	macrophage infecti
7	287	22.1	272	2 D81800	probable peptidyl-
8	279	21.5	243	2 A43596	mip protein - Legi
9	274.5	21.1	233	2 S22655	mip protein - Legi
10	273.5	21.1	233	2 S57924	macrophage infecti
11	263	20.2	253	2 H83238	probable peptidyl-
12	244.5	18.8	177	2 B87700	peptidyl-prolyl ci
13	240.5	18.5	259	2 D82331	peptidyl-prolyl ci
14	235.5	18.1	264	2 F71272	probable peptidyl-
15	233.5	18.0	270	2 F91153	fkbp-type peptidyl
16	233.5	18.0	270	2 I65035	fkbp-type peptidyl
17	230.5	17.7	241	2 B49992	peptidylprolyl iso
18	228.5	17.6	266	2 AF0024	peptidylprolyl iso
19	228.5	17.6	270	2 B85999	hypothetical prote
20	223	17.2	241	2 A64155	hypothetical prote
21	221.5	17.1	272	2 AD1004	peptidylprolyl iso
22	219	16.9	205	2 F83075	peptidyl-prolyl ci
23	212.5	16.4	209	2 F82060	peptidyl-prolyl ci
24	211	16.2	157	2 C82431	peptidyl-prolyl ci
25	201.5	15.5	259	2 S56432	peptidylprolyl iso
26	201.5	15.5	259	2 A98277	hypothetical prote
27	192.5	14.8	259	2 A86118	hypothetical prote
28	186	14.3	244	2 F90126	hypothetical prote
29	186	14.3	295	2 B82659	peptidyl-prolyl ci

30	185	14.2	206	2 AE0429	peptidylprolyl iso
31	185	14.2	220	2 AE1053	peptidylprolyl iso
32	174	13.4	178	2 T44823	probable macrophag
33	170.5	13.1	487	2 T10215	hypothetical prote
34	167	12.9	457	2 JC5422	FK506-binding prot
35	166.5	12.8	152	2 B75347	peptidyl-prolyl ci
36	163	12.5	568	2 T06489	probable peptidylp
37	161.5	12.4	109	2 E82022	peptidylprolyl iso
38	161.5	12.4	109	2 F81245	FKBP-type peptidyl
39	161	12.4	165	2 AH1878	FKBP-type peptidyl
40	160.5	12.4	196	1 S55332	macrophage infecti
41	160	12.3	201	1 S75144	FKBP-type peptidyl
42	159	12.2	120	2 S11090	FK506-binding prot
43	159	12.2	361	2 T43536	peptidyl-prolyl ci
44	158	12.2	114	2 G87595	peptidyl-prolyl ci
45	156.5	12.0	551	1 S72485	peptidylprolyl iso

ALIGNMENTS

RESULT 1  
F72052  
peptidyl-prolyl cis-trans isomerase Mip CP0086 [imported] - Chlamydoiphila pneumoniae (str: F72052)  
C:Species: Chlamydoiphila pneumoniae, Chlamydia pneumoniae  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: F72052; D81614  
R:Kallman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999  
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.  
A:Reference number: A72000; MUID:99206606; PMID:10192388  
A:Accession: F72052  
A:Molecule type: DNA  
A:Residues: 1-258 <ARN>  
A:Cross-references: UNIPROT:Q927P3; GB:AE001648; GB:AE001363; NID:G4376946; PIDN:AAD18801  
A:Experimental source: Strain CWL029  
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, I.; C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000  
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.  
A:Reference number: A81500; MUID:20150255; PMID:10684935  
A:Accession: D81614  
A:Molecule type: DNA  
A:Residues: 1-258 <REA>  
A:Cross-references: GB:AE002172; GB:AE002161; NID:G7189018; PIDN:AAF37972.1; PID:G7189021  
A:Experimental source: strain AR39, HL cells  
C:Genetics:  
A:Gene: mip; CP0086  
C:Superfamily: Escherichia coli peptidylprolyl isomerase fklB; BKBP-type peptidylprolyl is F:160-205/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>

Query Match	100.0%	Score 1299;	DB 2;	Length 258;
Best Local Similarity	100.0%;	Pred. No. 8.6e-84;		
Matches 258;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	MNRRLNLVATVALSASVSCDVRSKDKQDQGSLSVEYKDKNDIELSNQKLSRTFG	60
Db	1	MNRRLNLVATVALSASVSCDVRSKDKQDQGSLSVEYKDKNDIELSNQKLSRTFG	60
Qy	61	HLARQLRKSEDMFDDAEVAKGLQAEVLCKSAFLTETEEKMAEVOKLVPEKSKENL	120
Db	61	HLARQLRKSEDMFDDAEVAKGLQAEVLCKSAFLTETEEKMAEVOKLVPEKSKENL	120
Qy	121	SLAEKFLKENSKNAGVVEVQPSKLYKIIEKGAGKASGKPSALLHYKSGFINGQVFS	180
Db	121	SLAEKFLKENSKNAGVVEVQPSKLYKIIEKGAGKASGKPSALLHYKSGFINGQVFS	180
Qy	181	EGNNEPILLPLGQITPGFALGMQCKEGEIVLHPLDLAGTAGQLPPNSLLIPEINLI	240
Db	181	EGNNEPILLPLGQITPGFALGMQCKEGEIVLHPLDLAGTAGQLPPNSLLIPEINLI	240
Qy	241	QASADEVAAPQEGNQGE	258

Db 241 QASAEVAAPVQEGNOGE 258

RESULT 2

B86573

FKBP-type peptidyl-prolyl cis-trans isomerase [imported] - Chlamydomophila pneumoniae (strain J138)

C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae

C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C:Accession: B86573

R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ise, Nucleic Acids Res. 28, 2311-2314, 2000

A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.

A:Reference number: A86491; MUID:20330349; PMID:10871362

A:Accession: B86573

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-258 <STO>

A:Cross-references: EMBL:X66127; NID:g40701; PIDN:CAA46918.1; PID:g40702

A:Experimental source: strain J138

C:Genetics:

A:Gene: mip

C:Superfamily: Escherichia coli peptidylprolyl isomerase fklB; BKBP-type peptidylprolyl isomerase

Query Match 100.0%; Score 1299; DB 2; Length 258;

Best Local Similarity 100.0%; Pred. No. 8.6e-84;

Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNRNWLVLATVALALSVASCDVRSKDKDQGLVEYKDKNDTNDIELSDNOKLSRTFG 60

Db 1 MNRNWLVLATVALALSVASCDVRSKDKDQGLVEYKDKNDTNDIELSDNOKLSRTFG 60

QY 61 HLLARQLRSEDMFFDIAEVAKGLQALVCKSAPLTETEEYKMAEVQKLVFEKSKENL 120

Db 61 HLLARQLRSEDMFFDIAEVAKGLQALVCKSAPLTETEEYKMAEVQKLVFEKSKENL 120

QY 121 SLAEKFLKSNKAGVVEVQPSKQYKIIKEGAGKAISKPSALLHYKGSFINGQVFS 180

Db 121 SLAEKFLKSNKAGVVEVQPSKQYKIIKEGAGKAISKPSALLHYKGSFINGQVFS 180

QY 181 EGNNEPILLPLGQTIPGFALGQMGKEGTRVLIHPDLAYGTAGOLPNSLLIFEINLI 240

Db 181 EGNNEPILLPLGQTIPGFALGQMGKEGTRVLIHPDLAYGTAGOLPNSLLIFEINLI 240

QY 241 QASAEVAAPVQEGNOGE 258

Db 241 QASAEVAAPVQEGNOGE 258

RESULT 3

S28638

probable fklB-type peptidyl-prolyl cis-trans isomerase - Chlamydia trachomatis (serotype N)

N:Alternate names: mip-like protein

C:Species: Chlamydia trachomatis

C>Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004

C:Accession: S28638; S28639; D71503

R:Lundmose, A.G.

A:Title: Chlamydia trachomatis contains a protein similar to the Legionella pneumophila submitted to the EMBL Data Library, June 1992

A:Reference number: S28638

A:Accession: S28638

A:Molecule type: DNA

A:Residues: 1-243 <LUN>

A:Cross-references: UNIPROT:P26623; EMBL:X66128; NID:g40699; PIDN:CAA46919.1; PID:g40700

A:Experimental source: serotype B

C:Accession: S28639

A:Molecule type: DNA

A:Residues: 1-243 <LUN>

A:Cross-references: EMBL:X66127; NID:g40701; PIDN:CAA46918.1; PID:g40702

A:Experimental source: serotype E

R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998

A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis

A:Reference number: A71570; MUID:99000809; PMID:9784136

A:Accession: D71503

A:Molecule type: DNA

A:Residues: 1-243 <ARN>

A:Cross-references: GB:AE001324; GB:AE001273; NID:g3328966; PIDN:AAC68143.1; PID:g3328997;

A:Experimental source: serotype D, strain UW-3/Cx

C:Genetics:

A:Gene: mip

C:Superfamily: Escherichia coli peptidylprolyl isomerase fklB; BKBP-type peptidylprolyl isomerase

F:152-197/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>

Query Match 58.7%; Score 763; DB 2; Length 243;

Best Local Similarity 61.1%; Pred. No. 2.5e-46;

Matches 149; Conservative 36; Mismatches 49; Indels 10; Gaps 2;

QY 5 WNLVLATVALALSVASCDVRSKDKDQGLVEYKDKNDTNDIELSDNOKLSRTFGHLLA 64

Db 7 WMLMF---AVALPIVGC-----DNGGSGTSATEKSMVEDSALTDNOKLSRTFGHLLS 56

QY 65 ROLRSEDMFFDIAEVAKGLQALVCKSAPLTETEEYKMAEVQKLVFEKSKENLSLAE 124

Db 57 ROLSRTEDFSLDLVEIKGMQSEIDQSAPLTDTTEYKMAEVQKASFEAKCSENLSAE 116

QY 125 KFLKSNKAGVVEVQPSKQYKIIKEGAGKAISKPSALLHYKGSFINGQVFSSEGN 184

Db 117 KFLKSNKAGVVEVQPSKQYKIIKEGAGKAISKPSALLHYKGSFINGQVFSSEGN 176

QY 185 EPIILLPLGQTIPGFALGQMGKEGTRVLIHPDLAYGTAGOLPNSLLIFEINLIQASA 244

Db 177 EPIILLPLGQTIPGFALGQMGKEGTRVLIHPDLAYGTAGOLPNSLLIFEINLIQASA 236

QY 245 DEVA 248

Db 237 DNVS 240

RESULT 4

S25255

mip-like protein precursor - Chlamydia trachomatis

N:Alternate names: 27K membrane protein

C:Species: Chlamydia trachomatis

C>Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 09-Jul-2004

C:Accession: S25255; S15202

R:Lundmose, A.G.; Rouch, D.A.; Birkelund, S.; Christiansen, G.; Pearce, J.H. Mol. Microbiol. 6, 2539-2548, 1992

A:Title: Chlamydia trachomatis Mip-like protein.

A:Reference number: S25255; MUID:93023883; PMID:1406289

A:Accession: S25255

A:Molecule type: DNA

A:Residues: 1-243 <LUN>

A:Cross-references: UNIPROT:P26623; EMBL:X66126; NID:g40703; PIDN:CAA46917.1; PID:g40704

A:Note: this is a revision to the sequence from reference S15202

R:Lundmose, A.G.; Birkelund, S.; Fey, S.J.; Larsen, P.M.; Christiansen, G. Mol. Microbiol. 5, 109-115, 1991

A:Title: Chlamydia trachomatis contains a protein similar to the Legionella pneumophila

A:Reference number: S15202; MUID:91194539; PMID:2013997

A:Accession: S15202

A:Molecule type: DNA

A:Residues: 69-136, 'HD', 139-243 <LUN>

A:Cross-references: EMBL:X53481

A:Note: this sequence has been revised in reference S25255

C:Superfamily: Escherichia coli peptidylprolyl isomerase fklB; BKBP-type peptidylprolyl isomerase

C:Key words: membrane protein

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-243/Product: mip-like protein #status predicted <MAT>

F:152-197/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>

Query Match 58.7%; Score 762; DB 2; Length 243;

Best Local Similarity 61.1%; Pred. No. 3e-46;

Matches 149; Conservative 36; Mismatches 49; Indels 10; Gaps 2;

QY 5 WNLVLATVALALSVASCDVRSKDKDQGLVEYKDKNDTNDIELSDNOKLSRTFGHLLA 64

Db 7 WMLMF---AVALPIVGC-----DNGGSGTSATEKSMVEDSALTDNOKLSRTFGHLLA 56

Qy 65 RQLRKSEDMFFDIAEVAKGLQAEVLCKSAPLTETETEYBEKMAEVLQKLVFEKSKENLSLAE 124  
Db 57 RQLSRTEDFSLLDVEVINGMSEIDGOSAPLTDTEYEQMAEVLQKSAFQKSCSNLSAE 116  
Qy 125 KFLKENSKNAGVVEVQPSKLYKIIKEGAGKAISGKPSALLHYKGSFINGOVFSSESNN 184  
Db 117 EFLKENKEKAGVIELEPNKLYRVVKEGTGVLGSKPTALLHYTGSFIDGKVFOSSEKKN 176  
Qy 185 EPILLPLGQTTPGFALGMOGKEGTRVLYIHPDLAYGTAGQLPPNSLLIFEINLIQAS 244  
Db 177 EPILLPLTKVTPGFSQMGQKGEVRVLYIHPDLAYGTAGQLPPNSLLIFEVVKLEAND 236  
Qy 245 DEVA 248  
Db 237 DNVS 240

RESULT 5  
peptidyl-prolyl cis-trans isomerase Mip TC0828 [imported] - Chlamydia muridarum (strain D81660)  
C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn.  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 15-Jun-2001  
C:Accession: D81660  
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000  
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.  
A:Reference number: A81500; MUID:20150255; PMID:10684935  
A:Accession: D81660  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-261 <TET>  
A:Cross-references: GB:AE002349; GB:AE002160; NID:G7190851; PIDN:AAF39628.1; PID:G7190851  
A:Experimental source: strain Nigg (MoPn)  
C:Genetics:  
A:Gene: TC0828  
A:Superfamily: Escherichia coli peptidylprolyl isomerase fklB; BKBP-type peptidylprolyl is F:170-215/Domain: BKBP-type peptidylprolyl isomerase homology <ppi>

Query Match 56.4%; Score 733; DB 2; Length 261;  
Best Local Similarity 59.4%; Pred. No. 3.5e-44;  
Matches 145; Conservative 35; Mismatches 54; Indels 10; Gaps 2;  
Qy 5 WNLVLATVALALSASCDVRSKDKQDQGSLSVEYKDNKDTNDIELSDNQKLSRTFGHLLA 64  
Db 25 WMLMF--AVALPILGC-----DNNGSQTSAWGKDWVEDSVLTDNQKLSRTFGHLLA 74  
Qy 65 RQLRKSEDMFFDIAEVAKGLQAEVLCKSAPLTETETEYBEKMAEVLQKLVFEKSKENLSLAE 124  
Db 75 RQLSSTEDFTLDTLTVIKGMQSEIEGKSAPLTDSLEYETQMALVQKASFEKCKSENLSAE 134  
Qy 125 KFLKENSKNAGVVEVQPSKLYKIIKEGAGKAISGKPSALLHYKGSFINGOVFSSESNN 184  
Db 135 KFLKENKEGVIIEPNKLYRVVKEGTGVLGSKPTALLHYTGSFINGKRVDFSEKKN 194  
Qy 185 EPILLPLGQTTPGFALGMOGKEGTRVLYIHPDLAYGTAGQLPPNSLLIFEINLIQAS 244  
Db 195 DPILLPLTKVTPGFSQMGQKGEVRVLYIHPDLAYGTSGQLPPNSLLIFEVVKLEAND 254  
Qy 245 DEVA 248  
Db 255 DNVS 258

RESULT 6  
C81068  
macrophage infectivity potentiator NMB1567 [imported] - Neisseria meningitidis (strain M C:Species: Neisseria meningitidis  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C:Accession: C81068  
R:Jettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.

Science 287, 1809-1815, 2000  
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A:Reference number: A81000; MUID:20175755; PMID:10710307  
A:Accession: C81068  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-272 <TET>  
A:Cross-references: UNIPROT:Q9JYI8; GB:AE002507; GB:AE002098; NID:G7226811; PIDN:AAF41921  
A:Experimental source: serogroup B, strain MC58  
C:Genetics:  
A:Gene: NMB1567  
A:Superfamily: Escherichia coli peptidylprolyl isomerase fklB; BKBP-type peptidylprolyl is F:167-212/Domain: BKBP-type peptidylprolyl isomerase homology <ppi>

Query Match 22.9%; Score 297; DB 2; Length 272;  
Best Local Similarity 31.8%; Pred. No. 1.2e-13;  
Matches 84; Conservative 42; Mismatches 124; Indels 14; Gaps 6;  
Qy 1 MNRNRLVATVALALSASCDVRSKDKQDQGSLSVEYKDNKDTNDIELSDNQKLSRTFG 60  
Db 1 MNTIFKISALTLSAALALSACGKKEAAPASASEPAAASAAQDGTSSIG-STMQQASAYANG 59  
Qy 61 HLLARQLR--KSEDMFFDIAEVAKGLQAEVLCKSAPLTETETEYBEKMAEVLQKLVFEK 114  
Db 60 VDIGRSLKQMKEQGAIEDLVKVFTEAMQAVYDGKEIKMTEEQAEVMMKFLQEQQAQKAVEK 119  
Qy 115 ---KSKENLSLAERFLKENSKNAGVVEVQPSKLYKIIKEGAGKAISGKPSALLHYKGSF 171  
Db 120 HKADAKANKEGGEAFLEKNAKDG-VKTASGLQYKITQKQEGKQPTKDDIVTVEYEGRL 178  
Qy 172 INGQVFSSESNNPILLPGQTTPGFALGMOGKEGTRVLYIHPDLAY---GTAGQLP 228  
Db 179 IDGTVFDSKANGGVPVFPFLSQVTPGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIG 238  
Qy 229 PNSLLIFEINLIQASAEVAAPVQ 252  
Db 239 PNATLVDFDKVLKIGAPENAPAKQ 262

RESULT 7  
D81800  
probable peptidyl-prolyl isomerase NMA1756 [imported] - Neisseria meningitidis (strain Z: C:Species: Neisseria meningitidis  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004  
C:Accession: D81800  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell; Holroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z491.  
A:Reference number: A81775; MUID:20222556; PMID:10761919  
A:Accession: D81800  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-272 <PAR>  
A:Cross-references: UNIPROT:Q9JUT0; GB:AL162757; GB:AL157959; NID:G7380371; PIDN:CAB84984  
A:Experimental source: serogroup A, strain Z491  
C:Genetics:  
A:Gene: NMA1756  
A:Superfamily: Escherichia coli peptidylprolyl isomerase fklB; BKBP-type peptidylprolyl is F:167-212/Domain: BKBP-type peptidylprolyl isomerase homology <ppi>

Query Match 22.1%; Score 287; DB 2; Length 272;  
Best Local Similarity 31.4%; Pred. No. 5.9e-13;  
Matches 83; Conservative 42; Mismatches 125; Indels 14; Gaps 6;  
Qy 1 MNRNRLVATVALALSASCDVRSKDKQDQGSLSVEYKDNKDTNDIELSDNQKLSRTFG 60  
Db 1 MNTIFKISALTLSAALALSACGKKEAAPASASEPAAASAAQDGTSSIG-STMQQASAYANG 59  
Qy 61 HLLARQLR--KSEDMFFDIAEVAKGLQAEVLCKSAPLTETETEYBEKMAEVLQKLVFEK 114  
Db 60 VDIGRSLKQMKEQGAIEDLVKVFTEAMQAVYDGKEIKMTEEQAEVMMKFLQEQQAQKAVEK 119



Qy 231 SLLIFEINLI 240  
Db 218 ETLIFKIHLI 227

RESULT 11  
H83238  
probable peptidyl-prolyl cis-trans isomerase, Fkbp-type PA3262 [imported] - Pseudomonas  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C:Accession: H83238  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bz  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: H83238  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-253 <STO>  
A:Cross-references: UNIPROT:Q9HYX8; GB:AE004748; GB:AE004091; NID:g9949378; PIDN:AAG0665  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA3262  
C:Superfamily: Escherichia coli peptidylprolyl isomerase fklB; BKBP-type peptidylprolyl i

Query Match 20.2%; Score 263; DB 2; Length 253;  
Best Local Similarity 31.6%; Pred. No. 2.6e-11;  
Matches 77; Conservative 36; Mismatches 105; Indels 26; Gaps 5;

Qy 3 RRNLVLTVALSVASCDVRSDKDKDQGLVEYKDKNDTDELSDNOKLSRTFGLH 62  
Db 2 KOHLRAIALVGLVSCDSQTN-----VELK-----TPAQKASVIGLN 42

Qy 63 LARQLRKSEDMFFDIAEVAQLQAEVLCKAPLTETEEVEKMAEVQKLVFEKKS---KEN 119  
Db 43 MGKLSIQSGMDLDSKAVAKGIEDALGKKQQLTDEELTEAFALQKRAERMAAIGDEN 102

Qy 120 LSLAEKFLKENSAGVVEQVPSKLOYKIIKEGAGKASGKPSALLHYKSGFINGQVSS 179  
Db 103 AKAGKKFLKEGKRQGVTTASGLQYEVIVKADGQPKATDVVTVHYEGRLTGDTVFDS 161

Qy 180 SEGNNRILLPLGQTIPGALGMOQKGEETRVLVIHPDLAYGT---AGQLPPNSLLIFE 236  
Db 162 SIERGSPIDLPSGVIPGWEALQLMHVGEIKLYIPSELAYAGQSPSPAIPANSVLVFD 221

Qy 237 INLI 240  
Db 222 MELL 225

RESULT 12  
B87700  
peptidyl-prolyl cis-trans isomerase, FKBP-type [imported] - Caulobacter crescentus  
C:Species: Caulobacter crescentus  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
C:Accession: B87700  
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A:Title: Complete Genome Sequence of Caulobacter crescentus.  
A:Reference number: A87249; MUID:21173698; PMID:11259647  
A:Accession: B87700  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-177 <STO>  
A:Cross-references: UNIPROT:Q9A2C9; GB:AE005673; NID:gl13425390; PIDN:AAK25598.1; GSPDB:C  
C:Genetics:  
A:Gene: CC3636

Query Match 18.8%; Score 244.5; DB 2; Length 177;  
Best Local Similarity 38.1%; Pred. No. 3.3e-10;  
Matches 51; Conservative 28; Mismatches 50; Indels 5; Gaps 3;

Qy 114 KSKENLSLAEKFLKENSAGVVEQVPSKLOYKIIKEG--AGKAISGKPSALLHYKGSF 171  
Db 36 KKAQENLAADAFMAKNAKEFGVTL--PQGLQYKVRREGPNNGMHFNKVADEVKHYEGL 94

Qy 172 INGVFSSSEGNRPILLPLGQTIPGALGMOQKGEETRVLVIHPDLAYGT--AGQLPP 229  
Db 95 IDGTVFDSSYERGVPAVFPDLGLVPAMVIALQRMKAGDEWILYVPPALGYGAQDKGPIPG 154

Qy 230 NSLLIFEINLIQAS 243  
Db 155 NSVMIFRIELDVN 168

RESULT 13  
D82331  
peptidyl-prolyl cis-trans isomerase, FKBP-type VC0354 [imported] - Vibrio cholerae (strai  
C:Species: Vibrio cholerae  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C:Accession: D82331  
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.  
I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A:Reference number: A82035; MUID:20406833; PMID:10952301  
A:Accession: D82331  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-259 <HEI>  
A:Cross-references: UNIPROT:Q9KV04; GB:AE004124; GB:AE003852; NID:g9654770; PIDN:AAF9352;  
A:Experimental source: serogroup O1; strain N16961; biotype El Tor  
C:Genetics:  
A:Gene: VC0354  
A:Map position: 1  
C:Superfamily: Escherichia coli peptidylprolyl isomerase fklB; BKBP-type peptidylprolyl i

Query Match 18.5%; Score 240.5; DB 2; Length 259;  
Best Local Similarity 28.4%; Pred. No. 9.9e-10;  
Matches 75; Conservative 48; Mismatches 108; Indels 33; Gaps 9;

Qy 6 NLVLTVALSVASCDVRSDKDKD-----QGLSVEYK--DNKOTNDIELSDNOKLS 56  
Db 8 SLLAATVTLAV--GCQKEEAPKTETTPAAATAAKTVFEKSEDDKAAVAIGVS----- 58

Qy 57 RTFGHLLARQLRKSEDMFFDIAE--VAKGLQAEVLCKAPLTETE-----YEKMAEV 107  
Db 59 --FANYLKTSTIEKPSIEIGIDLNLKOLVLRKIE-HVFAGNPENMSEETRAALEALDKRVAET 115

Qy 108 QKLVFEKKSLENLSLAEKFLKENSAGVVEQVPSKLOYKIIKEGAGKASGKPSALLHY 167  
Db 116 MQAKAAEAENKKGDEFFRAQFEKSGVVKQT--SGLLYQVMTPAEGDKPKDQTDVQVHY 174

Qy 168 KGSFINGQVSSSGNNRPILLPLGQTIPGALGMOQKGEETRVLVIHPDLAYG--TAG 225  
Db 175 KGTLDIGSQFDSYERGERPATFPLNRVIPGVTGTEGVLMSVSGKFKLVIPPELAYGEQDTP 234

Qy 226 QLPNSLLIFEINLIQASAEVAA 249  
Db 235 TIPANSTLVFEVLLKIENGKDA 258

RESULT 14  
F71272  
probable peptidyl-prolyl cis-trans isomerase, FKBP-type, 22 kDa (fklB) - syphilis spiroch  
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)  
C:Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 09-Jul-2004  
C:Accession: F71272  
R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin  
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDor







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OM protein - protein search, using sw model

Run on: November 23, 2004, 12:12:32 ; Search time 144 Seconds  
(without alignments)  
634.479 Million cell updates/sec

Title: US-10-022-832-2

Perfect score: 1299

Sequence: 1 MNRWNLVATVALSVAS.....LIQASDAVEAAVPOEGNQGE 258

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*  
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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
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18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1299	100.0	258	14 US-10-022-832-2	Sequence 2, Appli
2	1299	100.0	258	15 US-10-312-273-55	Sequence 55, Appl
3	1299	100.0	258	15 US-10-289-762-699	Sequence 699, App
4	233	17.9	537	14 US-10-179-038-8	Sequence 8, Appli
5	226	17.4	239	11 US-09-809-665A-143	Sequence 143, App
6	194	14.9	390	14 US-10-389-493-10319	Sequence 10319, A
7	180.5	13.9	585	16 US-10-437-963-158013	Sequence 158013,
8	178.5	13.7	344	15 US-10-425-114-68360	Sequence 68360, A
9	171	13.2	553	14 US-10-310-154-496	Sequence 496, App
10	170.5	13.1	495	17 US-10-425-115-323715	Sequence 323715,
11	169	13.0	314	16 US-10-767-701-45023	Sequence 45023, A
12	168	12.9	230	14 US-10-369-493-8922	Sequence 8922, Ap
13	168	12.9	505	15 US-10-424-599-160002	Sequence 160002,

14	168	12.9	544	15	US-10-424-599-174536	Sequence 174536,
15	167	12.9	147	17	US-10-425-115-185116	Sequence 185116,
16	166.5	12.8	152	14	US-10-369-493-631	Sequence 631, App
17	166.5	12.8	601	16	US-10-437-963-141440	Sequence 141440,
18	161.5	12.4	588	17	US-10-425-115-367862	Sequence 367862,
19	159	12.2	107	9	US-09-751-100B-69	Sequence 69, Appli
20	159	12.2	107	9	US-09-751-100B-83	Sequence 83, Appli
21	158.5	12.2	634	17	US-10-425-115-210281	Sequence 210281,
22	156.5	12.0	410	15	US-10-425-114-51083	Sequence 51083, A
23	155.5	12.0	363	14	US-10-270-223-6	Sequence 6, Appli
24	153	11.8	327	16	US-10-408-765A-422	Sequence 422, App
25	151.5	11.7	134	17	US-10-425-115-268186	Sequence 268186,
26	151	11.6	548	15	US-10-424-599-223790	Sequence 223790,
27	150.5	11.6	230	14	US-10-341-967-111	Sequence 111, App
28	150	11.5	107	9	US-09-751-100B-82	Sequence 82, Appl
29	149.5	11.5	137	14	US-10-341-967-85	Sequence 85, Appl
30	149	11.5	483	14	US-10-270-223-2	Sequence 2, Appli
31	146.5	11.3	185	17	US-10-425-115-210428	Sequence 210428,
32	143.5	11.0	139	14	US-10-369-493-6160	Sequence 6160, Ap
33	143	11.0	107	9	US-09-751-100B-67	Sequence 67, Appl
34	143	11.0	107	9	US-09-751-100B-80	Sequence 80, Appl
35	143	11.0	108	10	US-09-970-561-4	Sequence 4, Appli
36	143	11.0	108	14	US-10-024-298A-121	Sequence 121, App
37	143	11.0	108	14	US-10-042-211A-121	Sequence 121, App
38	143	11.0	108	15	US-10-617-217A-121	Sequence 121, App
39	143	11.0	108	17	US-10-024-298A-121	Sequence 121, App
40	143	11.0	127	14	US-10-341-967-40	Sequence 40, Appl
41	143	11.0	127	14	US-10-341-967-72	Sequence 72, Appl
42	143	11.0	128	9	US-09-781-804-21	Sequence 21, Appl
43	143	11.0	128	15	US-10-716-062-21	Sequence 21, Appl
44	143	11.0	144	9	US-09-925-299-985	Sequence 985, App
45	143	11.0	144	10	US-09-925-299-985	Sequence 985, App

#### ALIGNMENTS

#### RESULT 1

US-10-022-832-2  
; Sequence 2, Application US/10022832  
; Publication No. US20030059896A1  
; GENERAL INFORMATION:  
; APPLICANT: COUTURE, FRANCE  
; APPLICANT: HAMEL, JOSEF  
; APPLICANT: BRODEUR, BERNARD R.  
; APPLICANT: MARTIN, DENIS  
; TITLE OF INVENTION: NOVEL CHLAMYDIA ANTIGENS AND CORRESPONDING DNA  
; TITLE OF INVENTION: FRAGMENTS  
; FILE REFERENCE: BIOVAC-15  
; CURRENT APPLICATION NUMBER: US/10/022.832  
; PRIOR FILING DATE: 2001-12-20  
; PRIOR FILING DATE: 2000-12-21  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 258  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
US-10-022-832-2

Query Match	100.0%	Score	1299;	DB	14;	Length	258;
Best Local Similarity	100.0%	Pred. No.	8e-109;				
Matches	258;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	MNRWNLVATVALSVASCDVRSKDKDQGSLSVEYKONKDTNDIELSDNQLSRFTG	60				
Db	1	MNRWNLVATVALSVASCDVRSKDKDQGSLSVEYKONKDTNDIELSDNQLSRFTG	60				
Qy	61	HLARQLRKSDMFDAIEAVAKGLQAEVLVCKSAPIETETEYEEKMAEVOKLVPEKSKENL	120				
Db	61	HLARQLRKSDMFDAIEAVAKGLQAEVLVCKSAPIETETEYEEKMAEVOKLVPEKSKENL	120				

QY 121 SLAEKFLKSNAGVVEQPSKQYKIIKEGAGKAIKSGKPSALLHYKGSFINGQVFS 180  
DB 121 SLAEKFLKSNAGVVEQPSKQYKIIKEGAGKAIKSGKPSALLHYKGSFINGQVFS 180  
QY 181 EGNNEPILLPGQTIPGFALGQMGKEGTRVLYIHPDLAYGTAGQLPPNSLLIFEINLI 240  
DB 181 EGNNEPILLPGQTIPGFALGQMGKEGTRVLYIHPDLAYGTAGQLPPNSLLIFEINLI 240  
QY 241 QASADEVAAPQEGNOGE 258  
DB 241 QASADEVAAPQEGNOGE 258

## RESULT 2

US-10-312-273-55  
; Sequence 55, Application US/10312273  
; Publication No. US20040005667A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SPA  
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE  
; FILE REFERENCE: P025035W0  
; CURRENT APPLICATION NUMBER: US/10/312,273  
; CURRENT FILING DATE: 2002-12-20  
; PRIOR APPLICATION NUMBER: 0016363.4  
; PRIOR FILING DATE: 2000-07-03  
; PRIOR APPLICATION NUMBER: 0017047.2  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 0017983.8  
; PRIOR FILING DATE: 2000-07-21  
; PRIOR APPLICATION NUMBER: 0019368.0  
; PRIOR FILING DATE: 2000-08-07  
; PRIOR APPLICATION NUMBER: 0020440.4  
; PRIOR FILING DATE: 2000-08-18  
; PRIOR APPLICATION NUMBER: 0022583.9  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 0027549.5  
; PRIOR FILING DATE: 2000-11-10  
; PRIOR APPLICATION NUMBER: 0031706.5  
; PRIOR FILING DATE: 2000-12-22  
; NUMBER OF SEQ ID NOS: 664  
; SOFTWARE: Seqwin99, version 1.02  
; SEQ ID NO 55  
; LENGTH: 258  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
US-10-312-273-55

Query Match 100.0%; Score 1299; DB 15; Length 258;  
Best Local Similarity 100.0%; Pred. No. 8e-109;  
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNRRLNLVATVALSALSVASCDVRSKDKQDQGSVLEVKDKNDTNDIELSDNQLSRFTG 60  
DB 1 MNRRLNLVATVALSALSVASCDVRSKDKQDQGSVLEVKDKNDTNDIELSDNQLSRFTG 60  
QY 61 HLLARQLRKSEDMFFDIAEVAKGLQAEVLVCKSAPLTETETEYEEKMAEVQKLVFEKSKENL 120  
DB 61 HLLARQLRKSEDMFFDIAEVAKGLQAEVLVCKSAPLTETETEYEEKMAEVQKLVFEKSKENL 120  
QY 121 SLAEKFLKSNAGVVEQPSKQYKIIKEGAGKAIKSGKPSALLHYKGSFINGQVFS 180  
DB 121 SLAEKFLKSNAGVVEQPSKQYKIIKEGAGKAIKSGKPSALLHYKGSFINGQVFS 180  
QY 181 EGNNEPILLPGQTIPGFALGQMGKEGTRVLYIHPDLAYGTAGQLPPNSLLIFEINLI 240  
DB 181 EGNNEPILLPGQTIPGFALGQMGKEGTRVLYIHPDLAYGTAGQLPPNSLLIFEINLI 240  
QY 241 QASADEVAAPQEGNOGE 258  
DB 241 QASADEVAAPQEGNOGE 258

## RESULT 3

Query Match 17.9%; Score 233; DB 14; Length 537;  
Best Local Similarity 28.3%; Pred. No. 3.7e-12;  
Matches 62; Conservative 53; Mismatches 86; Indels 18; Gaps 7;

US-10-289-762-699  
; Sequence 699, Application US/10289762  
; Publication No. US20040006218A1  
; GENERAL INFORMATION:  
; APPLICANT: Griffiths, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention, and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/10/289,762  
; CURRENT FILING DATE: 2003-03-27  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 699  
; LENGTH: 258  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
US-10-289-762-699

Query Match 100.0%; Score 1299; DB 15; Length 258;  
Best Local Similarity 100.0%; Pred. No. 8e-109;  
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNRRLNLVATVALSALSVASCDVRSKDKQDQGSVLEVKDKNDTNDIELSDNQLSRFTG 60  
DB 1 MNRRLNLVATVALSALSVASCDVRSKDKQDQGSVLEVKDKNDTNDIELSDNQLSRFTG 60  
QY 61 HLLARQLRKSEDMFFDIAEVAKGLQAEVLVCKSAPLTETETEYEEKMAEVQKLVFEKSKENL 120  
DB 61 HLLARQLRKSEDMFFDIAEVAKGLQAEVLVCKSAPLTETETEYEEKMAEVQKLVFEKSKENL 120  
QY 121 SLAEKFLKSNAGVVEQPSKQYKIIKEGAGKAIKSGKPSALLHYKGSFINGQVFS 180  
DB 121 SLAEKFLKSNAGVVEQPSKQYKIIKEGAGKAIKSGKPSALLHYKGSFINGQVFS 180  
QY 181 EGNNEPILLPGQTIPGFALGQMGKEGTRVLYIHPDLAYGTAGQLPPNSLLIFEINLI 240  
DB 181 EGNNEPILLPGQTIPGFALGQMGKEGTRVLYIHPDLAYGTAGQLPPNSLLIFEINLI 240  
QY 241 QASADEVAAPQEGNOGE 258  
DB 241 QASADEVAAPQEGNOGE 258

## RESULT 4

US-10-179-038-8  
; Sequence 8, Application US/10179038  
; Publication No. US20030096352A1  
; GENERAL INFORMATION:  
; Sequenzprotokoll  
; APPLICANT: Roche Diagnostics GmbH  
; APPLICANT: F. Hoffmann-La Roche AG  
; TITLE OF INVENTION: Use of FKBP chaperones as expression tool  
; FILE REFERENCE: 21306W0  
; CURRENT APPLICATION NUMBER: US/10/179,038  
; CURRENT FILING DATE: 2002-06-24  
; PRIOR APPLICATION NUMBER: EP01115225.3  
; PRIOR FILING DATE: 2001-06-22  
; PRIOR APPLICATION NUMBER: EP01120939.2  
; PRIOR FILING DATE: 2001-08-31  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 537  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: single-chain  
; OTHER INFORMATION: FKBP  
US-10-179-038-8

Query Match 17.9%; Score 233; DB 14; Length 537;  
Best Local Similarity 28.3%; Pred. No. 3.7e-12;  
Matches 62; Conservative 53; Mismatches 86; Indels 18; Gaps 7;

RESULT 6  
US-10-369-493-10319  
; Sequence 10319, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng

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Query Match      13.9%; Score 180.5; DB 16; Length 585;
Best Local Similarity 30.6%; Pred. No. 2.3e-07;
Matches 53; Conservative 34; Mismatches 63; Indels 23; Gaps 7;

Qy 101 EEKMAEVQKLVFEKKSKENSLAEKFLKRNKSNAGVVEQPSKLYQYIKKEGAG--KAIS 158
Db 15 EEVDVDMKDELDEGSSSPVAMKVGEK-----EIGKQRLKRLKKEGWDRPES 67

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; APPLICANT: Slater, Steven C.

00 121 ESUSFF11FFNRIUQF0VEUU 191

DD 121 ESGSFF11FFNAILQFDVELL 141

